GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 10:12:19 ; Search time 260.97 Seconds
(without alignments)
361.981 Million cell updates/sec

Title: US-10-717-984-1
Perfect score: 1149
Sequence: 1 MGKGDPKKPRGKMSSYAFFV.....DEEEEEDEEDEDEEEDDDDE 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1149	100.0	215	6	ABU07499	Abu07499 Protein d
2	1149	100.0	215	6	AAE35859	Aae35859 Human HMG
3	1149	100.0	215	7	ADD40789	Add40789 Human HMG
4	1149	100.0	215	7	ADD40788	Add40788 Human HMG
5	1149	100.0	215	7	ABM85677	Abm85677 Human pro
6	1149	100.0	215	8	ADO60491	Ado60491 Human hig
7	1149	100.0	215	8	ADO25918	Ado25918 Human hig
8	1149	100.0	215	8	ADO71477	Ado71477 Human hig
9	1149	100.0	215	8	ADR45922	Adr45922 Human hig
10	1149	100.0	215	8	ABM81508	Abm81508 Tumour-as
11	1149	100.0	215	9	ADW81011	Adw81011 Amphoteri
12	1149	100.0	215	9	ADX69343	Adx69343 Human amp
13	1149	100.0	215	9	ADY14248	Ady14248 PRO polyp
14	1149	100.0	215	9	ADY85326	Ady85326 Human hig
15	1149	100.0	215	9	ADY85085	Ady85085 Human HMG
16	1149	100.0	215	9	ADZ80804	Adz80804 Amino aci
17	1144	99.6	214	7	ADD47645	Add47645 Human Pro
18	1144	99.6	214	7	ADE60447	Ade60447 Human Pro
19	1144	99.6	214	7	ADE57980	Ade57980 Human Pro
20	1144	99.6	214	7	ADE57984	Ade57984 Human Pro
21	1144	99.6	214	7	ADE60732	Ade60732 Human Pro
22	1144	99.6	214	7	ADE60728	Ade60728 Human Pro
23	1144	99.6	214	8	ADS17580	Ads17580 Amino aci
24	1144	99.6	221	9	ADY85051	Ady85051 Human HMG
25	1142	99.4	215	5	ABB57220	Abb57220 Mouse isc
26	1142	99.4	215	6	AAE35860	Aae35860 Mouse and
27	1142	99.4	215	7	ADD47643	Add47643 Rat Prote
28	1142	99.4	215	8	ADO25919	Ado25919 Mouse/rat
29	1142	99.4	215	8	ADO71478	Ado71478 Mouse/rat
30	1142	99.4	215	8	ADR87104	Adr87104 High Mobi
31	1142	99.4	215	9	ADY85327	Ady85327 Mouse and
32	1142	99.4	220	7	ABM85676	Abm85676 Mouse pro
33	1142	99.4	252	9	ADY85016	Ady85016 Human HMG
34	1140	99.2	215	9	ADY85029	Ady85029 Rat and m
35	1140	99.2	215	9	ADY85088	Ady85088 Human HMG
36	1140	99.2	229	5	ABP64829	Abp64829 Human pro
37	1137	99.0	214	7	ADE60730	Ade60730 Rat Prote
38	1137	99.0	214	7	ADE57978	Ade57978 Rat Prote
39	1137	99.0	214	7	ADE57982	Ade57982 Rat Prote
40	1137	99.0	214	7	ADE60726	Ade60726 Rat Prote
41	1137	99.0	214	7	ADE60445	Ade60445 Rat Prote
42	1135	98.8	215	8	ADO80179	Ado80179 High mobi
43	1129	98.3	215	9	AEA90125	Aea90125 Human hig
44	1122.5	97.7	216	6	AAE35866	Aae35866 Human HMG
45	1122.5	97.7	216	8	ADO25935	Ado25935 Wild type

ALIGNMENTS

RESULT 1
ABU07499
ID ABU07499 standard; protein; 215 AA.
XX
AC ABU07499;
XX
DT 28-JAN-2003 (first entry)
XX
DE Protein differentially regulated in prostate cancer #102.
XX
KW Prostate cancer; gene expression; differential regulation;
KW molecular marker; drug target; cancer detection; cancer diagnosis;
KW cancer staging; cancer grading; cancer assessing; cancer monitoring.
XX
OS Homo sapiens.
XX
PN WO200281638-A2.
XX
PD 17-OCT-2002.
XX
PF 08-APR-2002; 2002WO-US010824.
XX
PR 06-APR-2001; 2001US-0281731P.
PR 06-APR-2001; 2001US-0281732P.
XX
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
XX
PI Sun Z, Jay G;
XX
DR WPI; 2003-058520/05.
DR N-PSDB; ABX10404.
XX
PT Novel genes which are differentially regulated in prostate cancer, useful
PT for diagnosing prostate cancer in prostate tissue sample and assessing
PT therapeutic or preventive intervention in prostate cancer patients.
XX
PS Claim 1; Page 413-414; 416pp; English.
XX
CC The invention describes genes (I) which are differentially regulated in
CC prostate cancer. (I) Is useful for diagnosing a prostate cancer in a
CC sample comprising prostate tissue, which involves determining the number
CC of target genes which are differentially-regulated in the sample, where
CC the number is indicative of the probability that the sample comprises
CC prostate cancer. (I) Is useful for assessing a therapeutic or preventive
CC intervention in a subject having a prostate cancer, which involves
CC determining the expression levels in a sample comprising prostate tissue
CC of target genes which are differentially-regulated in prostate cancer.

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CC   Preferably, the expression levels of at least 10 genes are determined.
CC   (I) is also useful for identifying agents that modulate a biological
CC   activity of a polypeptide differentially-regulated in prostate cancer
CC   cells, which involves contacting a polypeptide differentially-regulated
CC   in prostate cancer cells with a test agent under conditions effective for
CC   the test agent to modulate a biological activity of the polypeptide, and
CC   determining whether the test agent modulates the biological activity. (I)
CC   is useful as molecular markers, as drug targets, and for detecting,
CC   diagnosing, staging, grading, assessing, monitoring, prognosticating,
CC   preventing or treating, determining predisposition to diseases and
CC   conditions especially relating to prostate cancer. (I) and its expression
CC   products are used in the diagnostic test to assay for presence of cancer
CC   e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in
CC   blood etc. (I) is useful for assessing cancer e.g., to determine the type
CC   of cancer, its stage of development, the nature of genetic defect, etc.
CC   The polypeptide encoded by (I) can be used as target for therapy or drug
CC   discovery. (I) can also be used for expressing the polypeptide and thus
CC   for searching specific binding partners of the polypeptide. (I) is useful
CC   in therapeutic applications to treat prostate cancer. The identification
CC   of specific genes, and groups of genes, expressed in pathways
CC   physiologically relevant to prostate cancer permits the definition of
CC   functional and disease pathways and the delineation of targets in these
CC   pathways which are useful in diagnostic, therapeutic, and clinical
CC   applications. This is the amino acid sequence of a protein diferentially
CC   regulated in prostate cancer
XX
SQ   Sequence 215 AA;

  Query Match             100.0%;  Score 1149;  DB 6;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-93;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 2
AAE35859
ID   AAE35859 standard; protein; 215 AA.
XX
AC   AAE35859;
XX
DT   17-JUN-2003  (first entry)
XX
DE   Human HMG1 protein.
XX
KW   Human; high mobility group; HMG protein; HMG A box; HMG B box; asthma;
KW   inflammatory cytokine; endotoxic shock; rheumatoid arthritis; hepatitis;
KW   appendicitis; peptic ulcer; duodenal ulcer; Crohn's disease; meningitis;
KW   allergy; immune complex disease; sinusitis; bronchitis; atherosclerosis;
KW   emphysema; HIV infection; candidiasis; malaria; filariasis; myocarditis;
KW   Hodgkin's disease; neuritis; dermatitis; myocardial ischaemia; diabetes;
KW   Alzheimer's disease; Goodpasture's syndrome; graft-versus-host disease;
KW   amoebiasis; multiple sclerosis; gout; cerebral infarction; peritonitis;
KW   gene therapy; human immunodeficiency virus; HMGB1 protein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Binding-site    9. .85
FT                   /note= "DNA  binding motif (HMG1 A box)"
FT   Binding-site    89. .162
FT                   /note= "DNA  binding motif (HMG1 B box)"
XX
PN   WO200292004-A2.
XX
PD   21-NOV-2002.
XX
PF   15-MAY-2002; 2002WO-US015329.
XX
PR   15-MAY-2001; 2001US-0291034P.
XX
PA   (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (UYPI-) UNIV PITTSBURGH.
XX
PI   Tracey KJ,  Yang H,  Warren HS,  Fink MP;
XX
DR   WPI; 2003-120594/11.
XX
PT   New isolated polypeptide having a vertebrate HMG A box, useful for
PT   inhibiting a condition associated with an activated inflammatory cytokine
PT   cascade, e.g. endotoxic shock, myocardial infarction, asthma, HIV
PT   infection, malaria and diabetes.
XX
PS   Disclosure; Fig 12A; 82pp; English.
XX
CC   The invention relates to high mobility group (HMG) protein comprising DNA
CC   binding motifs termed HMG A box and HMG B box. HMG A box or a non-
CC   naturally occurring HMG A box inhibits the release of a pro-inflammatory
CC   cytokine from a vertebrate cell. The methods and compositions of the
CC   invention are useful for inhibiting a condition characterised by
CC   activation of an inflammatory cytokine cascade such as endotoxic shock,
CC   rheumatoid arthritis, appendicitis, peptic or duodenal ulcers, Crohn's
CC   disease, peritonitis, hepatitis, asthma, allergy, immune complex disease,
CC   sinusitis, bronchitis, emphysema, HIV infection, candidiasis, malaria,
CC   filariasis, amoebiasis, dermatitis, atherosclerosis, Alzheimer's disease,
CC   myocarditis, myocardial ischaemia, meningitis, multiple sclerosis, gout,
CC   cerebral infarction, neuritis, Goodpasture's syndrome, graft-versus-host
CC   disease, diabetes and Hodgkin's disease. The invention is useful in gene
CC   therapy. The present sequence is human HMG1 (also termed as HMGB1)
CC   protein
XX
SQ   Sequence 215 AA;

  Query Match             100.0%;  Score 1149;  DB 6;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-93;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 3
ADD40789
ID   ADD40789 standard; protein; 215 AA.
XX
AC   ADD40789;
XX
DT   15-JAN-2004  (first entry)
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XX
DE   Human HMGB1 protein #2.
XX
KW   high mobility group B protein; HMGB1; HMGB2; HMGB3; endometrial disease;
KW   contraceptive; endometrium; pregnancy; menstrual cycle irregularity;
KW   RAGE; receptor for advanced glycation end; gynaecological; cytostatic;
KW   nuclear transcription factor complex; tumour metastasis; endometriosis;
KW   polyps; hyperplasia; carcinoma.
XX
OS   Homo sapiens.
XX
PN   WO2003051383-A2.
XX
PD   26-JUN-2003.
XX
PF   19-DEC-2002; 2002WO-EP014579.
XX
PR   19-DEC-2001; 2001DE-01062556.
XX
PA   (ALCE-) ALCEDO BIOTECH GMBH.
XX
PI   Bullerdiek J;
XX
DR   WPI; 2003-505462/47.
XX
PT   Developing treatment and diagnosis of endometrial disorders, using high
PT   mobility group B proteins, or related nucleic acid or interaction
PT   partners, as targets.
XX
PS   Disclosure; SEQ ID NO 3; 43pp; German.
XX
CC   This invention describes a novel method comprising using high mobility
CC   group B proteins (HMGB) as target molecules for development or
CC   preparation of compositions (for treatment, prevention or diagnosis of
CC   endometrial diseases, or as contraceptives. The products of the invention
CC   are used in kit for characterising the status of the endometrium,
CC   especially for presence of pregnancy or irregularities in the menstrual
CC   cycle. The proteins used in the invention can be HMGB1, 2 or 3, or SP100-
CC   HMG, and the preferred interaction partner for HMGB1 is RAGE (receptor
CC   for advanced glycation end products). The products of the invention have
CC   gynaecological, contraceptive and cytostatic activity. HMGB is part of a
CC   nuclear transcription factor complex and, extracellularly, a ligand for
CC   the surface RAGE (receptor for advanced glycation end products) which is
CC   involved in tumour metastasis. The products of the invention are used to
CC   develop treatments, preventions or diagnoses of endometrial disease,
CC   particularly endometriosis or polyps, hyperplasia or carcinoma of the
CC   endometrium, also contraceptives and methods for assessing status of the
CC   endometrium, particularly for detecting pregnancy or menstrual disorders.
CC   This sequence represents the human HMGB1 protein used in the method of
CC   the invention.
XX
SQ   Sequence 215 AA;

  Query Match             100.0%;  Score 1149;  DB 7;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-93;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
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RESULT 4
ADD40788
ID   ADD40788 standard; protein; 215 AA.
XX
AC   ADD40788;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Human HMGB1 protein.
XX
KW   high mobility group B protein; HMGB1; HMGB2; HMGB3; endometrial disease;
KW   contraceptive; endometrium; pregnancy; menstrual cycle irregularity;
KW   RAGE; receptor for advanced glycation end; gynaecological; cytostatic;
KW   nuclear transcription factor complex; tumour metastasis; endometriosis;
KW   polyps; hyperplasia; carcinoma.
XX
OS   Homo sapiens.
XX
PN   WO2003051383-A2.
XX
PD   26-JUN-2003.
XX
PF   19-DEC-2002; 2002WO-EP014579.
XX
PR   19-DEC-2001; 2001DE-01062556.
XX
PA   (ALCE-) ALCEDO BIOTECH GMBH.
XX
PI   Bullerdiek J;
XX
DR   WPI; 2003-505462/47.
DR   N-PSDB; ADD40787.
XX
PT   Developing treatment and diagnosis of endometrial disorders, using high
PT   mobility group B proteins, or related nucleic acid or interaction
PT   partners, as targets.
XX
PS   Disclosure; Fig 4; 43pp; German.
XX
CC   This invention describes a novel method comprising using high mobility
CC   group B proteins (HMGB) as target molecules for development or
CC   preparation of compositions (for treatment, prevention or diagnosis of
CC   endometrial diseases, or as contraceptives. The products of the invention
CC   are used in kit for characterising the status of the endometrium,
CC   especially for presence of pregnancy or irregularities in the menstrual
CC   cycle. The proteins used in the invention can be HMGB1, 2 or 3, or SP100-
CC   HMG, and the preferred interaction partner for HMGB1 is RAGE (receptor
CC   for advanced glycation end products). The products of the invention have
CC   gynaecological, contraceptive and cytostatic activity. HMGB is part of a
CC   nuclear transcription factor complex and, extracellularly, a ligand for
CC   the surface RAGE (receptor for advanced glycation end products) which is
CC   involved in tumour metastasis. The products of the invention are used to
CC   develop treatments, preventions or diagnoses of endometrial disease,
CC   particularly endometriosis or polyps, hyperplasia or carcinoma of the
CC   endometrium, also contraceptives and methods for assessing status of the
CC   endometrium, particularly for detecting pregnancy or menstrual disorders.
CC   This sequence represents the human HMGB1 protein used in the method of
CC   the invention.
XX
SQ   Sequence 215 AA;

  Query Match             100.0%;  Score 1149;  DB 7;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-93;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
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Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 5
ABM85677
ID   ABM85677 standard; protein; 215 AA.
XX
AC   ABM85677;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human protein sequence hCP43793.
XX
KW   Cytostatic; carcinoma; lymphoma; cancer; human.
XX
OS   Homo sapiens.
XX
PN   WO2003073826-A2.
XX
PD   12-SEP-2003.
XX
PF   28-FEB-2003; 2003WO-US006235.
XX
PR   01-MAR-2002; 2002US-00087192.
XX
PA   (SAGR-) SAGRES DISCOVERY.
XX
PI   Morris DW;
XX
DR   WPI; 2003-328604/31.
XX
PT   Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
PT   comprises a nucleotide sequence.
XX
PS   Claim 5; SEQ ID NO 1446; 0pp; English.
XX
CC   The present invention relates to novel DNA and protein sequences which
CC   are associated with carcinomas. The sequences are useful for: (i) for
CC   screening drug candidates; (ii) for screening of bioactive agent capable
CC   of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
CC   a bioactive agent capable of modulating the activity of CAP; (iv) for
CC   evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
CC   carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
CC   carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
CC   (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
CC   determining Carcinoma Associated (CA) gene copy number. In addition, the
CC   CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC   carcinoma including lymphoma. The present sequence is one such CAP. Note:
CC   This patent is an equivalent to basic patent US2002182586A1, for which no
CC   sequence data was published
XX
SQ   Sequence 215 AA;

  Query Match            100.0%;  Score 1149;  DB 7;  Length 215;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-93;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 6
ADO60491
ID   ADO60491 standard; protein; 215 AA.
XX
AC   ADO60491;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Human high mobility group protein 1 (HMG1) protein SeqID2.
XX
KW   vaccine; amyloid beta 42 aggregation; amyloid beta 42 phagocytosis;
KW   microglia; high mobility group protein 1; HMG1; nootropic;
KW   neuroprotective; microglia; vaccine; Down's syndrome; amyloid angiopathy;
KW   brain amyloidosis; Alzheimer's disease; human.
XX
OS   Homo sapiens.
XX
PN   JP2004107260-A.
XX
PD   08-APR-2004.
XX
PF   18-SEP-2002; 2002JP-00272195.
XX
PR   18-SEP-2002; 2002JP-00272195.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
DR   WPI; 2004-343837/32.
DR   N-PSDB; ADO60490.
XX
PT   Vaccine for promoting amyloid beta 42 aggregation inhibitory effect
PT   and/or amyloid beta 42 phagocytosis, useful for prophylaxis and/or
PT   treatment of Alzheimer's disease or Down's syndrome, comprises high
PT   mobility group protein 1.
XX
PS   Disclosure; SEQ ID NO 2; 56pp; Japanese.
XX
CC   This invention relates to a novel vaccine for promoting amyloid beta 42
CC   aggregation inhibitory effect and/or amyloid beta 42 phagocytosis by
CC   microglia, which comprises a high mobility group protein 1 (HMG1), its
CC   partial peptide, or its salt. The invention may be useful for the
CC   production of compounds with a nootropic or neuroprotective activity
CC   acting as promoters of inhibition of amyloid beta 42 aggregation or
CC   promoters of amyloid beta 42 phagocytosis by microglia. The invention may
CC   also be useful for the production of a vaccine. The invention is useful
CC   for prophylaxis and/or treatment of Down's syndrome or amyloid angiopathy
CC   or preventing brain amyloidosis such as Alzheimer's disease. The present
CC   sequence is that of the protein encoded by the human high mobility group
CC   protein 1 (HMG1) gene which may be used during the creation of the novel
CC   vaccine of the invention.
XX
SQ   Sequence 215 AA;

  Query Match            100.0%;  Score 1149;  DB 8;  Length 215;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-93;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
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Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 7
ADO25918
ID   ADO25918 standard; protein; 215 AA.
XX
AC   ADO25918;
XX
DT   26-AUG-2004  (first entry)
XX
DE   Human high mobility group box 1 (HMG1).
XX
KW   cytostatic; gene therapy; vaccine; pharmaceutical composition;
KW   HMGB B box; high mobility group; immune response; immunostimulation;
KW   cancer; human; high mobility group box 1; HMG1; cytokine activity.
XX
OS   Homo sapiens.
XX
PN   WO2004046338-A2.
XX
PD   03-JUN-2004.
XX
PF   19-NOV-2003; 2003WO-US036975.
XX
PR   20-NOV-2002; 2002US-0427848P.
XX
PA   (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
XX
PI   Tracey KJ;
XX
DR   WPI; 2004-420625/39.
XX
PT   New pharmaceutical composition comprises a polypeptide comprising an HMGB
PT   B box or its functional variant, useful for stimulating or increasing an
PT   immune response in an individual or for treating cancer in an individual.
XX
PS   Disclosure; SEQ ID NO 1; 68pp; English.
XX
CC   The invention describes a pharmaceutical composition comprising a
CC   polypeptide comprising an HMGB (high mobility group box) B box or its
CC   functional variant to treat a disease or condition by increasing an
CC   immune response in an individual administered with the pharmaceutical
CC   composition. Also described are: an antibody attached to a polypeptide
CC   comprising an HMGB B box or its functional variant; stimulating or
CC   increasing an immune response in an individual in need of
CC   immunostimulation; and treating cancer in an individual. The composition
CC   is useful for stimulating or increasing an immune response in an
CC   individual in need of immunostimulation or for treating cancer in an
CC   individual. This is the amino acid sequence of human high mobility group
CC   box 1 (HMG1) that can be used to stimulate cytokine activity and increase
CC   immune response to assist in treating disease.
XX
SQ   Sequence 215 AA;

  Query Match             100.0%;  Score 1149;  DB 8;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-93;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
```

```
Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 8
ADO71477
ID   ADO71477 standard; protein; 215 AA.
XX
AC   ADO71477;
XX
DT   26-AUG-2004  (first entry)
XX
DE   Human high mobility group box 1 (HMGB1) protein #1.
XX
KW   Human; high mobility group box 1; HMGB1; HMGB; HMGB A box; HMGB B box;
KW   proinflammatory cytokine; weight loss; obesity; inflammation;
KW   inflammatory cytokine cascade; sepsis; allograft rejection;
KW   rheumatoid arthritis; asthma; lupus; adult respiratory distress syndrome;
KW   chronic obstructive pulmonary disease; psoriasis; pancreatitis;
KW   peritonitis; burn; myocardial ischaemia; organic ischaemia;
KW   reperfusion ischaemia; Behcet's disease; graft-versus-host disease;
KW   Crohn's disease; ulcerative colitis; multiple sclerosis; cachexia.
XX
OS   Homo sapiens.
XX
PN   WO2004046345-A2.
XX
PD   03-JUN-2004.
XX
PF   20-NOV-2003; 2003WO-US037507.
XX
PR   20-NOV-2002; 2002US-0427841P.
PR   20-NOV-2002; 2002US-0427846P.
XX
PA   (CRIT-) CRITICAL THERAPEUTICS INC.
XX
PI   Newman W,  O'keefe TL;
XX
DR   WPI; 2004-420628/39.
XX
PT   New high mobility group box proteins, useful in treating obesity, sepsis,
PT   rheumatoid arthritis, asthma, psoriasis, burns, myocardial ischemia,
PT   Behcet's disease, ulcerative colitis, multiple sclerosis, or cachexia.
XX
PS   Claim 29; SEQ ID NO 1; 113pp; English.
XX
CC   The invention relates to a polypeptide comprising a high mobility group
CC   box protein (HMGB) A or B box. The HMGB A or B box can inhibit release of
CC   a proinflammatory cytokine from a cell treated with an HMGB protein. The
CC   invention also relates to a purified preparation of antibodies that
CC   specifically bind to the HMGB B box but do not specifically bind to non-B
CC   box epitopes of HMGB, where the antibodies can inhibit release of a
CC   proinflammatory cytokine from a cell treated with HMGB, a method for
CC   effecting weight loss or treating obesity in a patient, a method of
CC   determining whether a compound inhibits inflammation, a pharmaceutical
CC   composition comprising an HMGB protein or an antibody that binds to the
CC   protein, an agent that inhibits TNF biological activity and a method of
CC   treating a condition in a patient characterised by activation of an
CC   inflammatory cytokine cascade. Effecting weight loss or treating obesity
CC   in a patient comprises administering to the patient an amount of the
CC   polypeptide. The polypeptide, antibodies, composition and methods are
CC   useful in treating obesity and conditions characterised by activation of
CC   an inflammatory cytokine cascade, e.g. sepsis, allograft rejection,
CC   rheumatoid arthritis, asthma, lupus, adult respiratory distress syndrome,
CC   chronic obstructive pulmonary disease, psoriasis, pancreatitis,
CC   peritonitis, burns, myocardial ischaemia, organic ischaemia, reperfusion
CC   ischaemia, Behcet's disease, graft-versus-host disease, Crohn's disease,
CC   ulcerative colitis, multiple sclerosis or cachexia. This sequence
```

CC represents a human HMGB1 polypeptide of the invention.
XX
SQ Sequence 215 AA;

Query Match 100.0%; Score 1149; DB 8; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.7e-93;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
Db 1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
Db 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy 121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
Db 121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy 181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
Db 181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215

RESULT 9
ADR45922
ID ADR45922 standard; protein; 215 AA.
XX
AC ADR45922;
XX
DT 21-OCT-2004 (first entry)
XX
DE Human high mobility group protein HMGB1 protein.
XX
KW antidiabetic; ophthalmological; nephropathic; antiarthritic;
KW antiinflammatory; cytostatic; gynaecological; antipsoriatic;
KW dermatological; antiviral; vasotropic; antiarteriosclerotic; antianginal;
KW cardiant; vulnerary; antiulcer; high mobility group protein; human.
XX
OS Homo sapiens.
XX
PN WO2004061456-A2.
XX
PD 22-JUL-2004.
XX
PF 05-JAN-2004; 2004WO-EP000030.
XX
PR 03-JAN-2003; 2003DE-01000023.
PR 07-MAR-2003; 2003DE-01010160.
PR 10-AUG-2003; 2003DE-01036642.
PR 08-OCT-2003; 2003DE-01046614.
XX
PA (ALCE-) ALCEDO BIOTECH GMBH.
XX
PI Bullerdiek J;
XX
DR WPI; 2004-571355/55.
DR N-PSDB; ADR45955, ADR45956.
XX
PT Use of nucleic acids encoding basic DNA-binding proteins, and their
PT translation or transcription products, for treating diseases associated
PT with e.g. angiogenesis, neovascularization or wound healing, also for
PT drug screening.
XX
PS Claim 57; SEQ ID NO 7; 161pp; German.
XX
CC The present invention relates to the use, especially in vitro, of nucleic
CC acids encoding high mobility group proteins for the following processes:
CC angiogenesis (including in a wound bed), neovascularization,
CC transmyocardial revascularization, wound healing, epithelialization and
CC healing in cases of tooth or bone implants. The sequences and their
CC encoded protein are useful for treating a very wide range of diseases:
CC (proliferative) diabetic retinopathy, diabetic nephropathy, macular
CC degeneration, arthritis, endometriosis, histiocytosis, psoriasis,
CC rosacea, eruptive or cavernous haemangioma, tumours (especially melanoma,
CC Kaposi sarcoma and basal cell carcinoma), haemorrhoids, arteriosclerosis,
CC angina pectoris, ischaemia, infarction, infertility, wounds (including
CC diabetic and other ulcers), also diseases associated with DNA damage,
CC especially xeroderma pigmentosum, 'leather skin', skin cancers and ageing
CC (including where associated with sunburn) and cardiac infarct, including
CC cosmetic treatment, especially as a sun-protection composition. Compounds
CC identified as modulators of the specified processes can also be used
CC therapeutically. The present sequence is a protein of the invention.
XX
SQ Sequence 215 AA;

Query Match 100.0%; Score 1149; DB 8; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.7e-93;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
Db 1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
Db 61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy 121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
Db 121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy 181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
Db 181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215

RESULT 10
ABM81508
ID ABM81508 standard; protein; 215 AA.
XX
AC ABM81508;
XX
DT 18-NOV-2004 (first entry)
XX
DE Tumour-associated antigenic target (TAT) polypeptide PRO71096, SEQ:3888.
XX
KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2004030615-A2.
XX
PD 15-APR-2004.
XX
PF 29-SEP-2003; 2003WO-US028547.
XX
PR 02-OCT-2002; 2002US-0414971P.
XX
PA (GETH) GENENTECH INC.
XX
PI Wu TD, Zhang Z, Zhou Y;
XX
DR WPI; 2004-347921/32.
DR N-PSDB; ACN39623.
XX
PT New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or

```
PT   prostate cancer or tumor.
XX
PS   Claim 12; SEQ ID NO 3888; 7273pp; English.
XX
CC   The invention relates to human tumour-associated antigenic target (TAT)
CC   polypeptides, and their related nucleic acids. The TAT polypeptides are
CC   overexpressed in cancer tissues compared to normal tissues, and may thus
CC   serve as effective targets for the diagnosis and treatment of cancer in
CC   mammals. The invention also relates to nucleic acid and polypeptide
CC   sequences at least 80% identical to the TAT nucleic acids and
CC   polypeptides; expression vectors and host cells comprising a TAT nucleic
CC   acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC   molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC   TAT polypeptide; and methods and compositions for the treatment or
CC   diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC   antibodies, antagonists, binding molecules and compositions are useful
CC   for diagnosing or treating a cell proliferative disorder associated with
CC   increased TAT expression, particularly cancers such as breast cancer,
CC   colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC   cancer, pancreatic cancer, cervical cancer, cancers of the central
CC   nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC   used as hybridisation probes, in chromosome and gene mapping, in
CC   chromosome identification and in gene therapy. The present sequence
CC   represents a TAT polypeptide of the invention
XX
SQ   Sequence 215 AA;

  Query Match             100.0%;  Score 1149;  DB 8;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-93;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 11
ADW81011
ID   ADW81011 standard; protein; 215 AA.
XX
AC   ADW81011;
XX
DT   21-APR-2005  (first entry)
XX
DE   Amphoterin protein sequence.
XX
KW   Vascular endothelial growth factor; VEGF;
KW   vascular endothelial growth factor receptor; VEGFR; dermatological;
KW   edema; gene therapy; vulnerary; injury; burn; skin cancer; cytostatic;
KW   wound healing; hematoma; pain; necrosis; ischemia; vasotropic;
KW   angiogenesis stimulation; vascularization; tissue regeneration;
KW   amphoterin.
XX
OS   Homo sapiens.
XX
PN   WO2005011722-A2.
XX
PD   10-FEB-2005.
XX
PF   14-JUN-2004; 2004WO-US019197.
XX
PR   12-JUN-2003; 2003US-0478114P.
PR   12-JUN-2003; 2003US-0478390P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
PA   (LICN ) LICENTIA LTD.
XX
PI   Alitalo K,  Saaristo A,  Karkkainen M,  Tammela T,  Asko-Seljavaara S;
PI   Yla-Herttuala S,  He Y;
XX
DR   WPI; 2005-142834/15.
XX
PT   Improving healing of skin graft or skin flap to underlying tissue useful
PT   in mastopexy, cosmetic surgery, abdominoplasty, involves using
PT   composition of vascular endothelial growth factor-C or D polynucleotides
PT   and/or polypeptides.
XX
PS   Example 11; SEQ ID NO 22; 119pp; English.
XX
CC   The present invention relates to new vascular endothelial growth factor
CC   (VEGF) proteins useful for skin healing of a skin graft onto underlying
CC   tissue. The method involves contacting a skin graft/flap or underlying
CC   tissue with an agent chosen from vascular endothelial growth factor C
CC   (VEGF-C) polynucleotides, VEGF-C polypeptides, VEGF-D polynucleotides,
CC   and VEGF-D polypeptides, in amount effective to reduce edema or increase
CC   perfusion at skin graft or flap. The composition comprises a gene therapy
CC   vector that encodes VEGF-C polynucleotide. The VEGF-C polypeptide
CC   comprises the formula X-B-Z or Z-B-X, where X binds VEGF receptor-3
CC   (VEGFR-3) and comprises a VEGFR-3 ligand amino acid sequence chosen from
CC   a prepro-VEGF-C sequence, and fragments that binds VEGFR-3, where Z
CC   comprises a heparin-binding amino acid sequence, and B comprises a
CC   covalent attachment linking X to Z. The VEGF-C polynucleotides, VEGF-C
CC   polypeptides, VEGF-D polynucleotides, and VEGF-D polypeptides comprise a
CC   VEGF homology domain (VHD) and a heparin-binding domain. Vulnerary. Gene
CC   therapy. The method is useful in treating skin injury such as burns or
CC   skin cancer, skin grafts, cosmetic surgery, a liposuction procedure, or
CC   in reconstructive surgery. The reconstructive surgery is breast
CC   reconstruction following mastectomy or injury. The subject is diabetic.
CC   The method is useful for improving post-surgical wound healing after
CC   reconstructive and cosmetic surgery and improves complications resulting
CC   from surgery which includes excessive bleeding, such as hematomas,
CC   bruising and wound-healing difficulties, pain, edema, necrosis and
CC   ischemia. The present sequence is amphoterin protein, which contains a
CC   heparin binding domain related to the invention.
XX
SQ   Sequence 215 AA;

  Query Match             100.0%;  Score 1149;  DB 9;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-93;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 12
ADX69343
ID   ADX69343 standard; protein; 215 AA.
XX
AC   ADX69343;
XX
```

DT 05-MAY-2005 (first entry)
XX
DE Human amphoterin.
XX
KW amphoterin; Heparin binding protein; Neuroprotective; Nootropic;
KW Antiparkinsonian; Anticonvulsant; VEGF-3 receptor;
KW Angiogenesis stimulator; Gene Therapy;
KW vascular endothelial growth factor receptor 3; VEGFR-3;
KW angiogenesis disorder; neurodegenerative disorder; Alzheimers disease;
KW Parkinsons disease; motor neurone disease; dementia; paralysis; VEGF-C;
KW neurological disease; Huntingtons chorea;
KW vascular endothelial growth factor receptor 3; neurological disease.
XX
OS Homo sapiens.
XX
PN WO2005016963-A2.
XX
PD 24-FEB-2005.
XX
PF 14-JUN-2004; 2004WO-US019122.
XX
PR 12-JUN-2003; 2003US-0478114P.
PR 12-JUN-2003; 2003US-0478390P.
PR 23-SEP-2003; 2003US-00669176.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
XX
PI Alitalo K, He Y, Tammela T;
XX
DR WPI; 2005-182331/19.
XX
PT New heparin-binding Vascular Endothelial Growth Factor Receptor 3 ligands
PT comprising prepro-VEGF-C, prepro-VEGF-D sequences or fragments, for
PT treating neurodegenerative disorder, e.g. Alzheimer's, Parkinson's, or
PT Huntington's disease.
XX
PS Disclosure; SEQ ID NO 63; 219pp; English.
XX
CC The invention relates to heparin-binding vascular endothelial growth
CC factor receptor 3 (VEGFR-3) proteins and encoding polynucleotides. The
CC heparin binding VEGFR-3 proteins are used for stimulating
CC lymphangiogenesis or angiogenesis in a mammal, and for modulating the
CC growth of mammalian endothelial cells, mammalian endothelial precursor
CC cells or hematopoietic progenitor cells. The polypeptide may also be used
CC for promoting recruitment, proliferation, differentiation, migration or
CC survival of neuronal cells or neuronal precursor cells, and for treating
CC neurodegenerative disorder, e.g. Alzheimer's diseases, Parkinson's
CC disease, Huntington's disease, motor neuron disease, Amyotrophic Lateral
CC Sclerosis (ALS), dementia, or cerebral palsy. The present sequence
CC represents human amphoterin.
XX
SQ Sequence 215 AA;

Query Match 100.0%; Score 1149; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.7e-93;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
```

RESULT 13
ADY14248
ID ADY14248 standard; protein; 215 AA.
XX
AC ADY14248;
XX
DT 05-MAY-2005 (first entry)
XX
DE PRO polypeptide SEQ ID NO 54.
XX
KW Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
KW Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;
KW Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;
KW Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
KW Antiallergic; ds; gene; diagnosis.
XX
OS Homo sapiens.
XX
PN WO2005016962-A2.
XX
PD 24-FEB-2005.
XX
PF 11-AUG-2004; 2004WO-US026249.
XX
PR 11-AUG-2003; 2003US-0493546P.
XX
PA (GETH) GENENTECH INC.
XX
PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;
XX
DR WPI; 2005-182330/19.
XX
PT New nucleic acid encoding PRO polypeptide, useful for diagnosing and
PT treating an immune related disorder, e.g. systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
XX
PS Claim 8; SEQ ID NO 54; 158pp; English.
XX
CC The invention relates to an isolated nucleic acid encoding a PRO
CC polypeptide. The polypeptide, agonist or an antagonist, antibody,
CC composition, and method are useful for diagnosing and treating an immune
CC related disorder, e.g. systemic lupus erythematosus, rheumatoid
CC arthritis. The present sequence represents a DNA encoding a PRO
CC polypeptide.
XX
SQ Sequence 215 AA;

Query Match 100.0%; Score 1149; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.7e-93;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
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RESULT 14
ADY85326
ID ADY85326 standard; protein; 215 AA.

```
XX
AC   ADY85326;
XX
DT   02-JUN-2005  (first entry)
XX
DE   Human high mobility group box protein HMGB1.
XX
KW   High mobility group box; HMGB1; immune disorder; infection;
KW   immunosuppressive; autoimmune disease; allergy; antiallergic;
KW   ulcerative colitis; antiinflammatory; antiulcer; gastrointestinal-gen.;
KW   Crohns disease; inflammation; asthma; antiasthmatic;
KW   rheumatoid arthritis; antirheumatic; antiarthritic; psoriasis;
KW   antipsoriatic; systemic lupus erythematosus; dermatological; antiulcer.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          32. .85
FT                   /label= A_box
FT   Region          93. .161
FT                   /label= B_box
XX
PN   WO2005025604-A2.
XX
PD   24-MAR-2005.
XX
PF   10-SEP-2004; 2004WO-US029540.
XX
PR   10-SEP-2003; 2003US-0502349P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
XX
PI   Warren HS,  Tracey KJ;
XX
DR   WPI; 2005-233421/24.
XX
PT   Treating an immune pathology in an individual comprises administering an
PT   amount of a high mobility group box (HMGB) polypeptide comprising a
PT   vertebrate or a non-naturally occurring HMGB A or B box, or its
PT   immunosuppressive fragment.
XX
PS   Claim 6; SEQ ID NO 1; 57pp; English.
XX
CC   The invention is based on the discovery that high mobility group box
CC   protein 1 (HMGB1, also known as high mobility group-1 or HMG1), when
CC   administered with an antigen, diminishes the antibody response to the
CC   administered antigen. HMGB1 has 2 DNA binding motifs, termed the A and B
CC   boxes. A claimed method of treating an immune pathology in an individual
CC   comprises administering a HMGB polypeptide comprising a vertebrate HMGB A
CC   box, a non-naturally-occurring HMGB A box, or an immunosuppressive
CC   fragment of the vertebrate or non-natural HMGB A box. The immune
CC   pathology is induced by the administration of a non-human antigen, non-
CC   self material (e.g. a cell or tissue such as bone marrow cells) or
CC   adjuvant to the individual, by the transplantation of an organ into the
CC   individual, or by infection from a microorganism. Claimed methods of
CC   protecting a subject against an immune pathology, inhibiting an immune
CC   pathology in an individual or decreasing an immune response to an
CC   administered non-human antigen comprise administering a HMGB polypeptide
CC   comprising a vertebrate HMGB A box, a non-naturally-occurring HMGB A box,
CC   or an immunosuppressive fragment of the vertebrate or non-natural A box.
CC   A claimed method of treating an autoimmune disorder in an individual
CC   comprises administering a HMGB polypeptide comprising a vertebrate HMGB A
CC   box, a non-naturally-occurring HMGB A box, or an immunosuppressive
CC   fragment of these, and a vertebrate or non-naturally-occurring HMGB B
CC   box. The HMGB polypeptide is preferably a HMGB1 peptide and may be
CC   truncated at the C-terminus. The autoimmune disease is allergy,
CC   ulcerative colitis, Crohn's disease, asthma, rheumatoid arthritis,
CC   psoriasis or systemic lupus erythematosus (all claimed). The present
CC   sequence is that of the human HMGB1 protein, which can be used as the
CC   HMGB polypeptide in methods of the invention.
XX
SQ   Sequence 215 AA;
```

```
  Query Match           100.0%;  Score 1149;  DB 9;  Length 215;
  Best Local Similarity  100.0%;  Pred. No. 2.7e-93;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
```

```
RESULT 15
ADY85085
ID   ADY85085 standard; protein; 215 AA.
XX
AC   ADY85085;
XX
DT   16-JUN-2005  (first entry)
XX
DE   Human HMGB1 A box.
XX
KW   High mobility group box; HMGB1; monoclonal antibody; antibody therapy;
KW   sepsis; antibacterial immunosuppressive; graft rejection; arthritis;
KW   antiarthritic; asthma; antiasthmatic; lupus erythematosus;
KW   antiinflammatory; inflammation; dermatological;
KW   respiratory distress syndrome; respiratory-gen.; psoriasis;
KW   antipsoriatic; chronic obstructive pulmonary disease; pancreatitis;
KW   peritonitis; burns; vulnerary; ischemia; vasotropic; Behcets disease;
KW   graft versus host disease; inflammatory bowel disease;
KW   gastrointestinal-gen.; multiple sclerosis neuroprotective; cachexia;
KW   anabolic; infection; musculoskeletal disease; immune disorder.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Rattus sp.
XX
PN   WO2005026209-A2.
XX
PD   24-MAR-2005.
XX
PF   10-SEP-2004; 2004WO-US029527.
XX
PR   11-SEP-2003; 2003US-0502568P.
XX
PA   (CRIT-) CRITICAL THERAPEUTICS INC.
XX
PI   Newman W,  Qin S,  Okeefe T,  Obar R;
XX
DR   WPI; 2005-233483/24.
XX
PT   New antibody or its antigen-binding fragment specific to a vertebrate
PT   high mobility group box (HMGB) A box that inhibits release of a
PT   proinflammatory cytokine from a cell treated with HMGB protein, useful
PT   for treating, e.g. sepsis.
XX
PS   Disclosure; SEQ ID NO 2; 123pp; English.
XX
CC   The invention provides antibodies, or their antigen-binding fragments,
CC   that bind to a vertebrate high mobility group box (HMGB) polypeptide, to
CC   methods of detecting and/or identifying an agent that binds to an HMGB
CC   polypeptide, methods of treating a condition in a subject characterized
CC   by activation of an inflammatory cytokine cascade, and methods of
```

CC detecting an HMGB polypeptide in a sample. The antibody (or antigen-
CC binding fragment) binds to a vertebrate HMGB A box but does not
CC specifically bind to non-A box epitopes of HMGB, and inhibits release of
CC a proinflammatory cytokine from a vertebrate cell treated with an HMGB
CC protein. A method of treating a condition characterized by activation of
CC an inflammatory cytokine cascade comprises administering an antibody of
CC the invention, or its antigen-binding fragment. The condition is selected
CC from sepsis, allograft rejection, arthritis, asthma, lupus, adult
CC respiratory distress syndrome, chronic obstructive pulmonary disease,
CC psoriasis, pancreatitis, peritonitis, burns, ischemia, Behcet's disease,
CC graft versus host disease, inflammatory bowel disease, multiple sclerosis
CC and cachexia, especially sepsis, arthritis, or lupus. The present
CC sequence is that of the A box of human HMGB1 ADY85012. An identical
CC sequence is also found in rat and mouse HMGB1.
XX
SQ Sequence 215 AA;

Query Match 100.0%; Score 1149; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.7e-93;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
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Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
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Search completed: April 6, 2006, 10:19:12
Job time : 263.97 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 10:19:38 ; Search time 41.0197 Seconds
(without alignments)
504.309 Million cell updates/sec

Title: US-10-717-984-1
Perfect score: 1149
Sequence: 1 MGKGDPKKPRGKMSSYAFFV.....DEEEEEDEEDEDEEEDDDDE 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1149	100.0	215	2	S02826	nonhistone chromos
2	1145	99.7	215	1	S01947	nonhistone chromos
3	1142	99.4	215	1	NSRTH1	nonhistone chromos
4	1142	99.4	215	2	I48688	non-histone chromo
5	1140	99.2	215	2	A28897	nonhistone chromos
6	1122.5	97.7	216	2	S29857	nonhistone chromos
7	984.5	85.7	210	2	S62355	high mobility grou
8	929	80.9	209	1	NSHUH2	nonhistone chromos
9	926.5	80.6	210	2	A34719	nonhistone chromos
10	919	80.0	210	2	S54774	high mobility grou
11	915	79.6	207	2	JC1114	high-mobility grou
12	905	78.8	207	2	JC1129	nonhistone chromos
13	894	77.8	170	2	A27853	nonhistone chromos
14	837.5	72.9	204	2	S48708	high-mobility-grou
15	830.5	72.3	204	2	T01071	high mobility grou
16	814.5	70.9	202	2	S22359	nonhistone chromos
17	813.5	70.8	205	2	S26062	nonhistone chromos
18	800	69.6	186	2	S30221	nonhistone chromos
19	799	69.5	201	2	I50254	HMG-1 - chicken
20	771	67.1	186	2	B61611	nonhistone chromos
21	755	65.7	215	2	I51067	gene HMG-T2 protei
22	686	59.7	172	2	A24019	nonhistone chromos
23	545	47.4	393	2	S50068	nonhistone chromos
24	544	47.3	393	2	JC6179	dorsal switch prot
25	489	42.6	200	2	JC4357	HMG1 protein - sea
26	372	32.4	202	2	E88479	protein F47D12.4 [
27	363	31.6	235	2	T43009	HMG protein 1.2 -
28	325.5	28.3	662	2	F86339	protein F2D10.18 [
29	311	27.1	168	2	T03640	high mobility grou
30	310	27.0	157	2	B47150	high mobility grou
31	289	25.2	178	2	T51159	HMG protein (impor
32	288.5	25.1	161	2	S18991	high mobility grou
33	278.5	24.2	502	2	T14286	embryogenic callus
34	271	23.6	54	2	S68823	HMG1 protein homol
35	268	23.3	141	2	T09581	probable high mobi
36	267.5	23.3	149	2	S39556	high mobility grou
37	264	23.0	144	2	S40302	high mobility grou
38	263.5	22.9	142	2	T02252	high mobility grou
39	259.5	22.6	708	2	A41265	DNA-binding protei
40	259	22.5	154	2	S40122	high mobility grou
41	255.5	22.2	669	2	S78050	high mobility grou
42	253.5	22.1	561	2	S35637	high mobility grou
43	251	21.8	709	2	A41976	structure-specific
44	250	21.8	446	2	T08187	hypothetical prote
45	249.5	21.7	144	2	T51597	high mobility grou

ALIGNMENTS

RESULT 1
S02826
nonhistone chromosomal protein HMG-1 - human
C;Species: Homo sapiens (man)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C;Accession: S02826; A33178; G33178
R;Wen, L.; Huang, J.K.; Johnson, B.H.; Reeck, G.R.
Nucleic Acids Res. 17, 1197-1214, 1989
A;Title: A human placental cDNA clone that encodes nonhistone chromosomal protein HMG-1.
A;Reference number: S02826; MUID:89160247; PMID:2922262
A;Accession: S02826
A;Molecule type: mRNA
A;Residues: 1-215 <WEN>
A;Cross-references: UNIPROT:P09429; UNIPARC:UPI00000015ED; EMBL:X12597; NID:g32326; PIDN
R;Ward, L.D.; Hong, J.; Whitehead, R.H.; Simpson, R.J.
Electrophoresis 11, 883-891, 1990
A;Title: Development of a database of amino acid sequences for human colon carcinoma pro
A;Reference number: A33178; MUID:91176935; PMID:2079031
A;Accession: A33178
A;Molecule type: protein
A;Residues: 2-13,'XXF' <WAR>
A;Cross-references: UNIPARC:UPI00001771D7
A;Accession: G33178
A;Molecule type: protein
A;Residues: 2-13,'XX',16-22 <WA2>
A;Cross-references: UNIPARC:UPI00001771D7
C;Genetics:
A;Gene: GDB:HMG1
A;Cross-references: GDB:133789; OMIM:163905
A;Map position: 13q12-13q12
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

Query Match 100.0%; Score 1149; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 9.2e-62;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
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                    ||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 2
S01947
nonhistone chromosomal protein HMG-1 - bovine
N;Alternate names: 33K protein; high-mobility-group protein HMG-1
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1989 #sequence_revision 22-Apr-1995 #text_change 09-Jul-2004
C;Accession: S01947; A61611; S10959; I45910
R;Kaplan, D.J.; Duncan, C.H.
Nucleic Acids Res. 16, 10375, 1988
A;Title: Full length cDNA sequence for bovine high mobility group 1 (HMG1) protein.
A;Reference number: S01947; MUID:89057489; PMID:3194213
A;Accession: S01947
A;Molecule type: mRNA
A;Residues: 1-215 <KAP>
A;Cross-references: UNIPROT:P10103; UNIPARC:UPI000016C31D; EMBL:X12796; NID:g416; PIDN:C
R;Walker, J.M.; Gooderham, K.; Hastings, J.R.B.; Mayes, E.; Johns, E.W.
FEBS Lett. 122, 264-270, 1980
A;Title: The primary structures of non-histone chromosomal proteins HMG 1 and 2.
A;Reference number: A61611; MUID:81138848; PMID:7202717
A;Accession: A61611
A;Molecule type: protein
A;Residues: 2-22,'S',24-40;48-105,'A',107-157,'X',160-193,'D',195 <WAL>
A;Cross-references: UNIPARC:UPI0000173987; UNIPARC:UPI0000173988
R;Christen, T.; Bischoff, M.; Hobi, R.; Kuenzle, C.C.
FEBS Lett. 267, 139-141, 1990
A;Title: High mobility group proteins 1 and 2 bind preferentially to brominated poly(dG-
A;Reference number: S10726; MUID:90306387; PMID:2365081
A;Accession: S10959
A;Molecule type: protein
A;Residues: 2-22,'X',24-38 <CHR>
A;Cross-references: UNIPARC:UPI0000173989
R;Pentecost, B.T.; Dixon, G.H.
Biosci. Rep. 4, 49-57, 1984
A;Title: Isolation and partial sequence of bovine cDNA clones for the high-mobility-grou
A;Reference number: I45910; MUID:84128872; PMID:6141822
A;Accession: I45910
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 'PGG',119,'V',121-215 <PEN>
A;Cross-references: UNIPARC:UPI000016C31E; GB:M26110; NID:g163156; PIDN:AAA30567.1; PID:
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; duplication; nucleus
F;2-215/Product: nonhistone chromosomal protein HMG-1 #status predicted <MAT>
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

  Query Match             99.7%;  Score 1145;  DB 1;  Length 215;
  Best Local Similarity   99.5%;  Pred. No. 1.6e-61;
  Matches  214;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||:||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEEEEDDDDE 215


RESULT 3
NSRTHI ~
nonhistone chromosomal protein HMG-1 - rat
N;Alternate names: 30K heparin-binding protein, brain; amphoterin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A41175; A27298; A30188; B48771; A48771; C48771
R;Merenmies, J.; Pihlaskari, R.; Laitinen, J.; Wartiovaara, J.; Rauvala, H.
J. Biol. Chem. 266, 16722-16729, 1991
A;Title: 30-kDa heparin-binding protein of brain (amphoterin) involved in neurite outgrov
A;Reference number: A41175; MUID:91358468; PMID:1885601
A;Accession: A41175
A;Molecule type: mRNA
A;Residues: 1-215 <MER>
A;Cross-references: UNIPROT:P07155; UNIPARC:UPI00000008A6; GB:M64986; NID:g202884; PIDN:A
A;Note: part of this sequence, including the amino end of the mature protein, was confirm
A;Note: the authors used antibodies to synthetic peptides to demonstrate this protein in
h-mobility group proteins
R;Paonessa, G.; Frank, R.; Cortese, R.
Nucleic Acids Res. 15, 9077, 1987
A;Title: Nucleotide sequence of rat liver HMG1 cDNA.
A;Reference number: A27298; MUID:88067717; PMID:3684582
A;Accession: A27298
A;Molecule type: mRNA
A;Residues: 1-10,'R',12-82,84-95,97,'AS',100-215 <PAO>
A;Cross-references: UNIPARC:UPI0000173984
R;Rauvala, H.; Merenmies, J.; Pihlaskari, R.; Korkolainen, M.; Huhtala, M.L.; Panula, P.
J. Cell Biol. 107, 2293-2305, 1988
A;Title: The adhesive and neurite-promoting molecule p30: analysis of the amino-terminal
 brain neurons.
A;Reference number: A30188; MUID:89066894; PMID:2461949
A;Accession: A30188
A;Molecule type: protein
A;Residues: 2-14,'X',16-21 <RAU>
A;Cross-references: UNIPARC:UPI0000173985
R;Parkkinen, J.; Raulo, E.; Merenmies, J.; Nolo, R.; Kajander, E.O.; Baumann, M.; Rauvala
J. Biol. Chem. 268, 19726-19738, 1993
A;Title: Amphoterin, the 30-kDa protein in a family of HMG1-type polypeptides. Enhanced e
A;Reference number: A48771; MUID:93374971; PMID:8366113
A;Accession: B48771
A;Status: preliminary
A;Molecule type: protein
A;Residues: 98-105,'X',107-112 <PA2>
A;Cross-references: UNIPARC:UPI0000173986
A;Experimental source: postnatal brain
A;Note: sequence extracted from NCBI backbone (NCBIP:137788)
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;2-215/Product: nonhistone chromosomal protein HMG-1 #status experimental <MAT>
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

  Query Match             99.4%;  Score 1142;  DB 1;  Length 215;
  Best Local Similarity   99.1%;  Pred. No. 2.4e-61;
  Matches  213;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||:|||||||||||||:||||||||||||
Db        181 SKKKKEEEDDEEDEEDEEEEEEEDEDEEEDDDDE 215


RESULT 4
I48688
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```
non-histone chromosomal high-mobility group 1 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48688; A55402; I57021
R;Yotov, W.V.; St-Arnaud, R.
Nucleic Acids Res. 20, 3516, 1992
A;Title: Nucleotide sequence of a mouse cDNA encoding the nonhistone chromosomal high mo
A;Reference number: I48687; MUID:92335012; PMID:1630928
A;Accession: I48688
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-215 <RES>
A;Cross-references: UNIPROT:P07155; UNIPARC:UPI00000008A6; EMBL:Z11997; NID:g53381; PIDN
R;Ferrari, S.; Ronfani, L.; Calogero, S.; Bianchi, M.E.
J. Biol. Chem. 269, 28803-28808, 1994
A;Title: The mouse gene coding for high mobility group 1 protein (HMG1).
A;Reference number: A55402; MUID:95050689; PMID:7961836
A;Accession: A55402
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-189,'E',191-215 <FER>
A;Cross-references: UNIPARC:UPI000016CDD6; EMBL:X80457; NID:g620097; PIDN:CAA56631.1; PI
R;Pauken, C.M.; Nagle, D.L.; Bucan, M.; Lo, C.W.
Mamm. Genome 5, 91-99, 1994
A;Title: Molecular cloning, expression analysis, and chromosomal localization of mouse H
A;Reference number: I57021; MUID:94235965; PMID:8180479
A;Accession: I57021
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-215 <RE2>
A;Cross-references: UNIPARC:UPI00000008A6; EMBL:U00431; NID:g437101; PIDN:AAA20508.1; PI
C;Genetics:
A;Gene: hmg1
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

  Query Match             99.4%;  Score 1142;  DB 2;  Length 215;
  Best Local Similarity   99.1%;  Pred. No. 2.4e-61;
  Matches  213;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              ||||||||:|||||||||||||:|||||||||||||
Db        181 SKKKKEEEDDEEDEEDEEEEEEEEDEDEEEDDDDE 215


RESULT 5
A28897
nonhistone chromosomal protein HMG-1 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: A28897
R;Tsuda, K.; Kikuchi, M.; Mori, K.; Waga, S.; Yoshida, M.
Biochemistry 27, 6159-6163, 1988
A;Title: Primary structure of non-histone protein HMG1 revealed by the nucleotide sequen
A;Reference number: A28897; MUID:89050965; PMID:3191113
A;Accession: A28897
A;Molecule type: mRNA
A;Residues: 1-215 <TSU>
A;Cross-references: UNIPROT:P12682; UNIPARC:UPI000016C6C4; GB:M21683; GB:M21684; NID:g16
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

  Query Match             99.2%;  Score 1140;  DB 2;  Length 215;
  Best Local Similarity   99.1%;  Pred. No. 3.2e-61;
  Matches  213;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKHPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
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Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEEEEDDDDE 215


RESULT 6
S29857
nonhistone chromosomal protein HMG-1 - human
C;Species: Homo sapiens (man)
C;Date: 08-Dec-1993 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C;Accession: S29857
R;Stros, M.; Dixon, G.H.
Biochim. Biophys. Acta 1172, 231-235, 1993
A;Title: A retropseudogene for non-histone chromosomal protein HMG-1.
A;Reference number: S29857; MUID:93176821; PMID:8439568
A;Accession: S29857
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-216 <STR>
A;Cross-references: UNIPARC:UPI000011DFAA; EMBL:L08048; NID:g184250; PIDN:AAA64970.1; PI
A;Note: the authors did not translate the codon for residue 1
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

  Query Match             97.7%;  Score 1122.5;  DB 2;  Length 216;
  Best Local Similarity   98.6%;  Pred. No. 3.5e-60;
  Matches  213;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
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Db          1 MGKGDPKKPTGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRLPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
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Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEED-EDEEEDDDDE 215
              |||||||||||||||||||||||| |||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEEEEDDDDE 216


RESULT 7
S62355
high mobility group protein 1 - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
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C;Accession: S62355
R;Nightingale, K.; Dimitrov, S.; Reeves, R.; Wolffe, A.P.
EMBO J. 15, 548-561, 1996
A;Title: Evidence for a shared structural role for HMG1 and linker histones B4 and H1 in
A;Reference number: S62355; MUID:96174815; PMID:8599938
A;Accession: S62355
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-210 <NIG>
A;Cross-references: UNIPROT:Q91596; UNIPARC:UPI00000FB3E3; EMBL:U21933; NID:g709958; PID
A;Note: the authors did not translate the codon for residue 1
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
F;6-82/Domain: HMG box homology <HMG1>
F;91-165/Domain: HMG box homology <HMG2>

  Query Match             85.7%;  Score 984.5;  DB 2;  Length 210;
  Best Local Similarity   83.7%;  Pred. No. 5.3e-52;
  Matches  180;  Conservative   20;  Mismatches   10;  Indels    5;  Gaps    2;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              |||||||||||||||||:|||||||||||||||||||:||||||||||||||| ||| ||
Db          1 MGKGDPKKPRGKMSSYAYFVQTCREEHKKKHPDASVNFAEFSKKCSERWKTMS-KEKTKF 59

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              |||||||| |||||||:||||||||||:||||||||||||||||||::||||||||||
Db         60 EDMAKADKVRYEREMKSYIPPKGETKKRFKDPNAPKRPPSAFFLFCSDFRPKIKGEHPGS 119

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
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Db        120 TIGDIAKKLGEMWNNTATDDKLPYERRAAKLKEKYEKDVAAYRAKGKPEPAKKAPAKPEK 179

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              :|||:||:||    :||||:::||||:||||||||
Db        180 AKKKEEEDED----DDEEEDDEEEDEEEEEDDDDE 210


RESULT 8
NSHUH2
nonhistone chromosomal protein HMG-2 - human
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: A42425; S20061; S18068
R;Shirakawa, H.; Yoshida, M.
J. Biol. Chem. 267, 6641-6645, 1992
A;Title: Structure of a gene coding for human HMG2 protein.
A;Reference number: A42425; MUID:92202209; PMID:1551873
A;Accession: A42425
A;Molecule type: DNA
A;Residues: 2-209 <SHI>
A;Cross-references: UNIPROT:P26583; UNIPARC:UPI000012CA25; GB:M83665; NID:g184235; PIDN:
A;Note: sequence extracted from NCBI backbone (NCBIN:89899, NCBIP:89900)
A;Note: initiator Met not shown
R;Majumdar, A.; Brown, D.; Kerby, S.; Rudzinski, I.; Polte, T.; Randhawa, Z.; Seidman, M
Nucleic Acids Res. 19, 6643, 1991
A;Title: Sequence of human HMG2 cDNA.
A;Reference number: S20061; MUID:92093633; PMID:1754403
A;Accession: S20061
A;Molecule type: mRNA
A;Residues: 1-209 <MAJ>
A;Cross-references: UNIPARC:UPI000013E34D; EMBL:X62534; NID:g32332; PIDN:CAA44395.1; PID
C;Genetics:
A;Gene: GDB:NHCP2
A;Cross-references: GDB:119451; OMIM:118880
A;Map position: 7pter-7qter
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

  Query Match             80.9%;  Score 929;  DB 1;  Length 209;
  Best Local Similarity   81.3%;  Pred. No. 1e-48;
  Matches  170;  Conservative   19;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              |||||| |||||||||||||||||||||||||:||||:|||||||||||||||| ||
Db          1 MGKGDPNKPRGKMSSYAFFVQTCREEHKKKHPDSSVNFAEFSKKCSERWKTMSAKEKSKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              |||||:|||||:|||| |:|||| | | |||||||||||||||||:||||| |||||
Db         61 EDMAKSDKARYDREMKNYVPPKGDKKGKKKDPNAPKRPPSAFFLFCSEHRPKIKSEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
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Db        121 SIGDTAKKLGEMWSEQSAKDKQPYEQKAAKLKEKYEKDIAAYRAKGKSEAGKKGPGRPTG 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEE 209
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Db        181 SKKKNEPEDEEEEEEEEDEDEEEEDEDEE 209


RESULT 9
A34719
nonhistone chromosomal protein HMG-2 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 09-Jul-2004
C;Accession: A34719
R;Shirakawa, H.; Tsuda, K.; Yoshida, M.
Biochemistry 29, 4419-4423, 1990
A;Title: Primary structure of non-histone chromosomal protein HMG2 revealed by the nucle
A;Reference number: A34719; MUID:90275208; PMID:2350545
A;Accession: A34719
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-210 <SHI>
A;Cross-references: UNIPROT:P17741; UNIPARC:UPI000016C6C5; GB:J02895; NID:g164491; PIDN:
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

  Query Match             80.6%;  Score 926.5;  DB 2;  Length 210;
  Best Local Similarity   81.5%;  Pred. No. 1.5e-48;
  Matches  172;  Conservative   18;  Mismatches   20;  Indels    1;  Gaps    1;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              |||||| |||||||||||||||||||||||||:||||:|||||||||||||||| ||
Db          1 MGKGDPNKPRGKMSSYAFFVQTCREEHKKKHPDSSVNFAEFSKKCSERWKTMSAKEKSKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              |||||:|||||:|||| |:|||| | | |||||||||||||||||:||||| |||||
Db         61 EDMAKSDKARYDREMKNYVPPKGDKKGKKKDPNAPKRPPSAFFLFCSEHRPKIKSEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
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Db        121 SIGDTAKKLGEMWSEQSAKDKQPYEQKAAKLKEKYEKDIAAYRAKGKGEAGKKGPGRPTG 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEED 211
              | ||| | ||||:||:|||:||||:|||:|:
Db        181 S-KKKNEPEDEEEEEEEEEDEDEEEEDEDEE 210


RESULT 10
S54774
high mobility group 2 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S54774; S52211
R;Zwilling, S.; Koenig, H.; Wirth, T.
EMBO J. 14, 1198-1208, 1995
A;Title: High mobility group protein 2 functionally interacts with the POU domains of oct
A;Reference number: S54774; MUID:95237201; PMID:7720710
A;Accession: S54774
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-210 <ZWI>
A;Cross-references: UNIPROT:P30681; UNIPARC:UPI000016432C; EMBL:Z46757; NID:g609168; PIDN
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C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

Query Match 80.0%; Score 919; DB 2; Length 210;
Best Local Similarity 80.5%; Pred. No. 4.1e-48;
Matches 169; Conservative 20; Mismatches 21; Indels 0; Gaps 0;

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Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              |||||| |||||||||||||||||||||||||:||||:||||||||||||||||||  ||
Db          1 MGKGDPNKPRGKMSSYAFFVQTCREEHKKKHPDSSVNFAEFSKKCSERWKTMSAKEKSKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||:||:|||||:|||| |:||||: | | ||||||||||||||||||| ||||| |||||
Db         61 EDLAKSDKARYDREMKNYVPPKGDKKGKKKDPNAPKRPPSAFFLFCSENRPKIKIEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              |||| |||||||:  :| ||||||:|||||||||||||||||||| :| |||  :
Db        121 SIGDTAKKLGEMWSEQSAKDKQPYEQKAAKLKEKYEKDIAAYRAKGKSEAGKKGPGRPTG 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEE 210
              |||| | |::||:||:||||:|||:|::||
Db        181 SKKKNEPEDEEEEEEEEEEEDDEEEEEDEE 210
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RESULT 11
JC1114
high-mobility group protein 2 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004
C;Accession: JC1114
R;Davis, D.L.; Burch, J.B.E.
Gene 113, 251-256, 1992
A;Title: Isolation of a chicken HMG2 cDNA clone and evidence for an HMG2-specific 3'-unt
A;Reference number: JC1114; MUID:92241676; PMID:1572546
A;Accession: JC1114
A;Molecule type: mRNA
A;Residues: 1-207 <DAV>
A;Cross-references: UNIPROT:P26584; UNIPARC:UPI0000171347; GB:M83235; NID:g211926; PIDN:
C;Comment: The high mobility group proteins are among the most abundant nonhistone chrom
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

Query Match 79.6%; Score 915; DB 2; Length 207;
Best Local Similarity 81.2%; Pred. No. 7e-48;
Matches 168; Conservative 17; Mismatches 22; Indels 0; Gaps 0;

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Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              |||||| ||||||||||:|||||||||||||||:||||:|||:||||||||||:||||||
Db          1 MGKGDPNKPRGKMSSYAYFVQTCREEHKKKHPDSSVNFAEFSRKCSERWKTMSSKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              |:||| |||||:|||| |:||||| | | ||||||||||||||||||:||||| :||||
Db         61 EEMAKGDKARYDREMKNYVPPKGEKKGKKKDPNAPKRPPSAFFLFCSEHRPKIKNDHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              |||| |||||||:   | ||||||:||||||||||||||||| | || |||  :
Db        121 SIGDTAKKLGEMWSEQLAKDKQPYEQKAAKLKEKYEKDIAAYRAKSKSDAGKKGPGRPAG 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDED 207
              |||| | ||:||:||||||||:||||:
Db        181 SKKKAEPEEEEEEEEDEEEEEEEEDEE 207
```

RESULT 12
JC1129
nonhistone chromosomal protein HMG-2 - chicken
N;Alternate names: high-mobility-group protein 2
C;Species: Gallus gallus (chicken)
C;Date: 05-Mar-1993 #sequence_revision 05-Mar-1993 #text_change 09-Jul-2004
C;Accession: JC1129
R;Sparrow, D.B.; Wells, J.R.E.
Gene 114, 289-290, 1992
A;Title: Sequence of a cDNA encoding chicken high-mobility-group protein-2.
A;Reference number: JC1129; MUID:92290291; PMID:1601311
A;Accession: JC1129
A;Molecule type: mRNA
A;Residues: 1-207 <SPA>
A;Cross-references: UNIPROT:P26584; UNIPARC:UPI0000171348; GB:M80574; NID:g211928; PIDN:
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

Query Match 78.8%; Score 905; DB 2; Length 207;
Best Local Similarity 80.2%; Pred. No. 2.8e-47;
Matches 166; Conservative 18; Mismatches 23; Indels 0; Gaps 0;

```
Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              |||||| ||||||||||:|||||  ||||||||:||||:|||:||||||||||:||||||
Db          1 MGKGDPNKPRGKMSSYAYFVQTCPREHKKKHPDSSVNFAEFSRKCSERWKTMSSKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              |:||| |||||:|||| |:||||| | | ||||||||||||||||||:||||| :||||
Db         61 EEMAKGDKARYDREMKNYVPPKGEKKGKKKDPNAPKRPPSAFFLFCSEHRPKIKNDHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              |||| |||||||:   :| ||||||:|||||||||||||||||| | || |||  :
Db        121 SIGDTAKKLGEMWSEQSAKDKQPYEQKAAKLKEKYEKDIAAYRAKSKSDAGKKGPGRPAG 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDED 207
              |||| | ||:||:|||||||||:||||:
Db        181 SKKKAEPEEEEEEEEDEEEEEEEEDEE 207
```

RESULT 13
A27853
nonhistone chromosomal protein HMG-1 - Chinese hamster (fragment)
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: A27853
R;Lee, K.L.D.; Pentecost, B.T.; D'Anna, J.A.; Tobey, R.A.; Gurley, L.R.; Dixon, G.H.
Nucleic Acids Res. 15, 5051-5068, 1987
A;Title: Characterization of cDNA sequences corresponding to three distinct HMG-1 mRNA s
A;Reference number: A27853; MUID:87259986; PMID:3601666
A;Accession: A27853
A;Molecule type: mRNA
A;Residues: 1-170 <LEE>
A;Cross-references: UNIPROT:P07156; UNIPARC:UPI00001771D5
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;1-38/Domain: HMG box homology (fragment) <HMG1>
F;47-121/Domain: HMG box homology <HMG2>

Query Match 77.8%; Score 894; DB 2; Length 170;
Best Local Similarity 98.8%; Pred. No. 1e-46;
Matches 168; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy         46 SERWKTMSAKEKGKFEDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLF 105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 SERWKTMSAKEKGKFEDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLF 60

Qy        106 CSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAK 165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAK 120

Qy        166 GKPDAAKKGVVKAEKSKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||:|||||||||||:|||||||||||||
Db        121 GKPDAAKKGVVKAEKSKKKKEEEDDEEDEEDEEEEEEEEDEDEEEDDDDE 170
```

RESULT 14
S48708
high-mobility-group-1 protein - trout

```
C;Species: Salmo sp. (trout)
C;Date: 01-Aug-1995 #sequence_revision 19-Apr-1996 #text_change 07-May-1999
C;Accession: S48708
R;Stros, M.; Nishikawa, S.; Dixon, G.H.
Eur. J. Biochem. 225, 581-591, 1994
A;Title: cDNA sequence and structure of a gene encoding trout testis high-mobility-group
A;Reference number: S48708; MUID:95045507; PMID:7957172
A;Accession: S48708
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-204 <STR>
A;Cross-references: UNIPARC:UPI00001771D9
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
F;5-82/Domain: HMG box homology <HMG1>
F;91-165/Domain: HMG box homology <HMG2>

  Query Match             72.9%;  Score 837.5;  DB 2;  Length 204;
  Best Local Similarity   71.8%;  Pred. No. 2.8e-43;
  Matches  150;  Conservative   34;  Mismatches   20;  Indels    5;  Gaps    2;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||| ||:||||||||||:|||||| |||||||:|||||||||||||||||||||||||||
Db          1 MGK-DPRKPRGKMSSYAYFVQTCRIEHKKKHPEASVNFSEFSKKCSERWKTMSAKEKGKF 59

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||:|| || ||||||::|||||||| ||:|||||||||| ||||:||:::||::||| |||
Db         60 EDLAKLDKVRYEREMRSYIPPKGEKKKRFKDPNAPKRPSSAFFIFCADFRPQVKGETPGL 119

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              |||||||||||| |||  |:|| ||||||:|||||||||| ||| |||   :    : |:
Db        120 SIGDVAKKLGEKWNNLTAEDKVPYEKKASKLKEKYEKDITAYRNKGKVPVS----MPAKA 175

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEE 209
              :   |::::|::|::|:|:::|::|||:|
Db        176 AAPAKDDDDDDDDDDDDEDDDDDDDEDDE 204


RESULT 15
T01071
high mobility group protein T - rainbow trout
N;Alternate names: HMG-T protein
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01071
R;Pentecost, B.T.; Wright, J.M.; Dixon, G.H.
Nucleic Acids Res. 13, 4871-4888, 1985
A;Title: Isolation and sequence of cDNA clones coding for a member of the family of high
A;Reference number: A24019; MUID:85269614; PMID:4022777
A;Accession: T01071
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-204 <PEN>
A;Cross-references: UNIPROT:P07746; UNIPARC:UPI000012CA3E; EMBL:X02666; NID:g64327; PIDN
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
F;91-165/Domain: HMG box homology <HMG>

  Query Match             72.3%;  Score 830.5;  DB 2;  Length 204;
  Best Local Similarity   71.3%;  Pred. No. 7.3e-43;
  Matches  149;  Conservative   35;  Mismatches   20;  Indels    5;  Gaps    2;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||| ||:||||||||||:|||| |||||||||:|||||||||||||||||||||||||||
Db          1 MGK-DPRKPRGKMSSYAYFVQTRREEHKKKHPEASVNFSEFSKKCSERWKTMSAKEKGKF 59

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||:|| || ||||||::||||||| ||:|||||||||| ||||:||:::||::||| |||
Db         60 EDLAKLDKVRYEREMRSYIPPKGEKKKRFKDPNAPKRPSSAFFIFCADFRPQVKGETPGL 119

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              |||||||||||| |||  |:|| ||||||::||||||||| ||| |||   :    : |:
Db        120 SIGDVAKKLGEKWNNLTAEDKVPYEKKASRLKEKYEKDITAYRNKGKVPVS----MPAKA 175

Qy    ' - 181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEE 209
              :   |::::|::|::|:|:::|::|||:|
Db        176 AAPAKDDDDDDDDDDDDEDDDDDDDEDDE 204

Search completed: April  6, 2006, 10:26:18
Job time : 42.0197 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 10:13:48 ; Search time 253.898 Seconds
(without alignments)
597.439 Million cell updates/sec

Title: US-10-717-984-1
Perfect score: 1149
Sequence: 1 MGKGDPKKPRGKMSSYAFFV.....DEEEEEDEEDEDEEEDDDDE 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1149	100.0	215	2	Q5T7C3_HUMAN	Q5t7c3 homo sapien
2	1149	100.0	215	2	Q4R844_MACFA	Q4r844 macaca fasc
3	1145	99.7	215	2	Q9QX40_SPAEH	Q9qx40 spalax leuc
4	1144	99.6	214	1	HMG1_CANFA	Q6yka4 canis famil
5	1144	99.6	214	1	HMG1_HUMAN	P09429 homo sapien
6	1142	99.4	215	2	Q9QWY6_SPAEH	Q9qwy6 spalax leuc
7	1142	99.4	215	2	Q548R9_RAT	Q548r9 rattus norv
8	1142	99.4	215	2	Q58EV5_MOUSE	Q58ev5 m high mobi
9	1140	99.2	214	1	HMG1_BOVIN	P10103 bos taurus
10	1139	99.1	215	2	O88611_SPAEH	O88611 spalax leuc
11	1138	99.0	215	2	O88612_SPAEH	O88612 spalax leuc
12	1137	99.0	214	1	HMG1_MOUSE	P63158 mus musculu
13	1137	99.0	214	1	HMG1_RAT	P63159 rattus norv
14	1136	98.9	215	2	Q6P202_MOUSE	Q6p202 mus musculu
15	1135	98.8	214	1	HMG1_PIG	P12682 sus scrofa
16	1129	98.3	215	2	Q14321_HUMAN	Q14321 homo sapien
17	1125	97.9	215	2	Q8BQ02_MOUSE	Q8bq02 mus musculu
18	1067	92.9	215	2	Q9YH06_CHICK	Q9yh06 gallus gall
19	1061.5	92.4	214	2	Q9PUK9_CHICK	Q9puk9 gallus gall
20	1061	92.3	211	2	Q9NQJ4_HUMAN	Q9nqj4 homo sapien
21	1050.5	91.4	211	1	HMG1X_HUMAN	Q9ugv6 homo sapien
22	1025	89.2	192	2	Q5T7C5_HUMAN	Q5t7c5 homo sapien
23	1005	87.5	211	2	Q6P4N5_XENTR	Q6p4n5 xenopus tro
24	1001	87.1	211	2	Q7SZ42_XENLA	Q7sz42 xenopus lae
25	996	86.7	206	2	Q5BKQ1_MOUSE	Q5bkq1 mus musculu
26	984.5	85.7	210	2	Q91596_XENLA	Q91596 xenopus lae
27	981.5	85.4	210	2	Q6GNQ5_XENLA	Q6gnq5 xenopus lae
28	969	84.3	181	2	Q8BNM0_MOUSE	Q8bnm0 mus musculu
29	955	83.1	178	2	Q8C7C4_MOUSE	Q8c7c4 mus musculu
30	948	82.5	180	1	HMG1_CRIGR	P07156 cricetulus
31	929	80.9	209	2	Q5U072_HUMAN	Q5u072 homo sapien
32	924	80.4	208	1	HMG2_HUMAN	P26583 homo sapien
33	921.5	80.2	209	1	HMG2_PIG	P17741 sus scrofa
34	920.5	80.1	208	2	Q5U071_HUMAN	Q5u071 homo sapien
35	917.5	79.9	210	2	Q5FVP0_RAT	Q5fvp0 rattus norv
36	914	79.5	209	1	HMG2_MOUSE	P30681 mus musculu
37	912.5	79.4	209	1	HMG2_RAT	P52925 rattus norv
38	910	79.2	206	1	HMG2_CHICK	P26584 gallus gall
39	894.5	77.9	212	2	Q8AVU3_XENLA	Q8avu3 xenopus lae
40	893	77.7	191	2	Q75MM1_HUMAN	Q75mm1 homo sapien
41	892	77.6	212	2	Q7ZXK5_XENLA	Q7zxk5 xenopus lae
42	885.5	77.1	205	2	Q7ZVC6_BRARE	Q7zvc6 brachydanio
43	884.5	77.0	212	2	Q6P7M9_XENTR	Q6p7m9 xenopus tro
44	881.5	76.7	205	2	Q6NX86_BRARE	Q6nx86 brachydanio
45	873	76.0	212	2	Q91764_XENLA	Q91764 xenopus lae

ALIGNMENTS

RESULT 1
Q5T7C3_HUMAN
ID Q5T7C3_HUMAN PRELIMINARY; PRT; 215 AA.
AC Q5T7C3;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE High-mobility group box 1.
GN Name=HMGB1; ORFNames=RP11-550P23.1-004;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Pelan S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AL353648; CAI15600.1; -; Genomic_DNA.
DR GO; GO:0000785; C:chromatin; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
SQ SEQUENCE 215 AA; 24894 MW; 8A868CF277D417B5 CRC64;

Query Match 100.0%; Score 1149; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 6.9e-59;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
```

RESULT 2
Q4R844_MACFA
ID Q4R844_MACFA PRELIMINARY; PRT; 215 AA.
AC Q4R844;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Testis cDNA clone: QtsA-13487, similar to human high-mobility group

```
DE   box 1 (HMGB1),.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   International consortium for macaque cDNA sequencing, analysis;
RT   "DNA sequences of macaque genes expressed in brain or testis and its
RT   evolutionary implications.";
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
RA   Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.;
RT   "Substitution rate and structural divergence of 5'UTR evolution:
RT   Comparative analysis between human and cynomolgus monkey cDNAs.";
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB168615; BAE00728.1; -; mRNA.
SQ   SEQUENCE   215 AA;  24894 MW;  8A868CF277D417B5 CRC64;

  Query Match             100.0%;  Score 1149;  DB 2;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 6.9e-59;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 3
Q9QX40_SPAEH
ID   Q9QX40_SPAEH PRELIMINARY;      PRT;   215 AA.
AC   Q9QX40;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   High mobility group protein.
GN   Name=HMG1;
OS   Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Spalacinae; Nannospalax.
OX   NCBI_TaxID=30637;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Lee K.-L.D., Lum H.-K., Nevo E.;
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF078820; AAC27653.2; -; Genomic_DNA.
DR   HSSP; P07156; 1NHN.
DR   SMR; Q9QX40; 2-84, 93-171.
DR   GO; GO:0000785; C:chromatin; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
SQ   SEQUENCE   215 AA;  24895 MW;  599FB8A6FDF41F17 CRC64;

  Query Match             99.7%;  Score 1145;  DB 2;  Length 215;
  Best Local Similarity   99.5%;  Pred. No. 1.2e-58;
  Matches  214;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAEEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 4
HMG1_CANFA
ID   HMG1_CANFA     STANDARD;      PRT;   214 AA.
AC   Q6YKA4;
DT   10-MAY-2005 (Rel. 47, Created)
DT   10-MAY-2005 (Rel. 47, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   High mobility group protein 1 (HMG-1) (High mobility group protein
DE   B1).
GN   Name=HMGB1;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC   Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA].
RX   MEDLINE=22932580; PubMed=14571134; DOI=10.1159/000073415;
RA   Murua Escobar H., Meyer B., Richter A., Becker K., Flohr A.M.,
RA   Bullerdiek J., Nolte I.;
RT   "Molecular characterization of the canine HMGB1.";
RL   Cytogenet. Genome Res. 101:33-38(2003).
CC   -!- FUNCTION: Binds preferentially single-stranded DNA and unwinds
CC       double stranded DNA (By similarity).
CC   -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC   -!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
CC   -!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; AY135519; AAN11296.1; -; mRNA.
DR   EMBL; AY135521; AAN11319.1; -; Genomic_DNA.
DR   HSSP; P07155; 1AAB.
DR   SMR; Q6YKA4; 1-83, 92-170.
DR   Ensembl; ENSCAFG00000006597; Canis familiaris.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
KW   Chromosomal protein; DNA-binding; Nuclear protein; Repeat.
FT   INIT_MET      0      0       By similarity.
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```
FT   DNA_BIND      8     78       HMG box 1.
FT   DNA_BIND     94    162       HMG box 2.
FT   COMPBIAS    185    214       Asp/Glu-rich (acidic).
SQ   SEQUENCE   214 AA;  24763 MW;  B3C6A80FC7F0F433 CRC64;

  Query Match             99.6%;  Score 1144;  DB 1;  Length 214;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-58;
  Matches  214;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 60

Qy         62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 120

Qy        122 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 180

Qy        182 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||
Db        181 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 214


RESULT 5
HMG1_HUMAN
ID   HMG1_HUMAN     STANDARD;      PRT;   214 AA.
AC   P09429; Q6IBE1;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-AUG-1990 (Rel. 15, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   High mobility group protein 1 (HMG-1) (High mobility group protein
DE   B1).
GN   Name=HMGB1; Synonyms=HMG1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=89160247; PubMed=2922262;
RA   Wen L., Huang J.K., Johnson B.H., Reeck G.R.;
RT   "A human placental cDNA clone that encodes nonhistone chromosomal
RT   protein HMG-1.";
RL   Nucleic Acids Res. 17:1197-1214(1989).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX   MEDLINE=96299787; PubMed=8661151; DOI=10.1006/geno.1996.0369;
RA   Ferrari S., Finelli P., Rocchi M., Bianchi M.E.;
RT   "The active gene that encodes human high mobility group 1 protein
RT   (HMG1) contains introns and maps to chromosome 13.";
RL   Genomics 35:367-371(1996).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RA   He F.T., Yang Z.H., Ji Q., Li R., Peng J., Jiang Y., Zhong X.;
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Small intestine;
RG   The German cDNA consortium;
RL   Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA   Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RT   "Cloning of human full open reading frames in Gateway(TM) system entry
RT   vector (pDONR201).";
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA   Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA   Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA   Phelan M., Farmer A.;
RT   "Cloning of human full-length CDSs in BD Creator(TM) system donor
RT   vector.";
RL   Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Brain, Cervix, and Testis;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [8]
RP   PROTEIN SEQUENCE OF 57-64 AND 112-126.
RC   TISSUE=Mammary carcinoma;
RX   MEDLINE=97295304; PubMed=9150946;
RA   Rasmussen R.K., Ji H., Eddes J.S., Moritz R.L., Reid G.E.,
RA   Simpson R.J., Dorow D.S.;
RT   "Two-dimensional electrophoretic analysis of human breast carcinoma
RT   proteins: mapping of proteins that bind to the SH3 domain of mixed
RT   lineage kinase MLK2.";
RL   Electrophoresis 18:588-598(1997).
CC   -!- FUNCTION: Binds preferentially single-stranded DNA and unwinds
CC       double stranded DNA.
CC   -!- INTERACTION:
CC       P04637:TP53; NbExp=1; IntAct=EBI-389432, EBI-366083;
CC       O15350:TP73; NbExp=1; IntAct=EBI-389432, EBI-389606;
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
CC   -!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; X12597; CAA31110.1; -; mRNA.
DR   EMBL; U51677; AAB08987.1; -; Genomic_DNA.
DR   EMBL; AY377859; AAQ91389.1; -; mRNA.
DR   EMBL; CR749614; CAH18408.1; -; mRNA.
DR   EMBL; CR456863; CAG33144.1; -; mRNA.
DR   EMBL; BT006940; AAP35586.1; -; mRNA.
DR   EMBL; BT020159; AAV38961.1; -; mRNA.
DR   EMBL; BC003378; AAH03378.1; -; mRNA.
DR   EMBL; BC030981; AAH30981.1; -; mRNA.
DR   EMBL; BC066889; AAH66889.1; -; mRNA.
DR   EMBL; BC067732; AAH67732.1; -; mRNA.
DR   PIR; S02826; S02826.
DR   HSSP; P07156; 1NHN.
DR   SMR; P09429; 1-83, 92-170.
DR   IntAct; P09429; -.
DR   Ensembl; ENSG00000189403; Homo sapiens.
DR   HGNC; HGNC:4983; HMGB1.
DR   H-InvDB; HIX0011209; -.
DR   MIM; 163905; -.
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DR   GO; GO:0000793; C:condensed chromosome; IDA.
DR   GO; GO:0008301; F:DNA bending activity; TAS.
DR   GO; GO:0008134; F:transcription factor binding; TAS.
DR   GO; GO:0006288; P:base-excision repair, DNA ligation; IDA.
DR   GO; GO:0006310; P:DNA recombination; TAS.
DR   GO; GO:0006281; P:DNA repair; TAS.
DR   GO; GO:0006268; P:DNA unwinding; NAS.
DR   GO; GO:0006325; P:establishment and/or maintenance of chromat. . .; TAS.
DR   GO; GO:0017055; P:negative regulation of transcriptional prei. . .; IDA.
DR   GO; GO:0006357; P:regulation of transcription from RNA polyme. . .; IDA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
KW   Chromosomal protein; Direct protein sequencing; DNA-binding;
KW   Nuclear protein; Repeat.
FT   INIT_MET      0      0
FT   DNA_BIND      8     78       HMG box 1.
FT   DNA_BIND     94    162       HMG box 2.
FT   COMPBIAS    185    214       Asp/Glu-rich (acidic).
FT   CONFLICT    214    214       E -> D (in Ref. 5).
SQ   SEQUENCE   214 AA;  24763 MW;  B3C6A80FC7F0F433 CRC64;

  Query Match             99.6%;  Score 1144;  DB 1;  Length 214;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-58;
  Matches  214;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 60

Qy         62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 120

Qy        122 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 180

Qy        182 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||
Db        181 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 214


RESULT 6
Q9QWY6_SPAEH
ID   Q9QWY6_SPAEH PRELIMINARY;      PRT;   215 AA.
AC   Q9QWY6;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   High mobility group protein.
GN   Name=HMG1;
OS   Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Spalacinae; Nannospalax.
OX   NCBI_TaxID=30637;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Lee K.-L.D., Lum H.-K., Nevo E.;
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF078819; AAC27652.1; -; Genomic_DNA.
DR   HSSP; P07156; 1NHN.
DR   SMR; Q9QWY6; 2-84, 93-171.
DR   GO; GO:0000785; C:chromatin; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
SQ   SEQUENCE   215 AA;  24822 MW;  D20D659274B575B4 CRC64;

  Query Match             99.4%;  Score 1142;  DB 2;  Length 215;
  Best Local Similarity   99.5%;  Pred. No. 1.8e-58;
  Matches  214;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREGHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 7
Q548R9_RAT
ID   Q548R9_RAT  PRELIMINARY;      PRT;   215 AA.
AC   Q548R9;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Amphoterin.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sprague-Dawley; TISSUE=Kidney;
RA   Ito T., Suzuki A., Horimoto N., Imai E., Hori M.;
RT   "Amphoterin is associated with the development of the kidney.";
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF275734; AAF82799.1; -; mRNA.
SQ   SEQUENCE   215 AA;  24894 MW;  8A868DE266D552B5 CRC64;

  Query Match             99.4%;  Score 1142;  DB 2;  Length 215;
  Best Local Similarity   99.1%;  Pred. No. 1.8e-58;
  Matches  213;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              ||||||||:|||||||||||:|||||||||||||
Db        181 SKKKKEEEDDEEDEEDEEEEEEEDEDEEEDDDDE 215


RESULT 8
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Q58EV5_MOUSE
ID   Q58EV5_MOUSE PRELIMINARY;      PRT;   215 AA.
AC   Q58EV5;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   High mobility group box 1 (16 days neonate thymus cDNA, RIKEN full-
DE   length enriched library, clone:A130064K11 product:high mobility group
DE   box 1, full insert sequence) (13 days embryo heart cDNA, RIKEN full-
DE   length enriched library, clone:D330050N16 product:high mobility group
DE   box 1, full insert sequence).
GN   Name=Hmgb1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Colon, and Mammary tumor. C3;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Colon;
RG   NIH MGC Project;
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RG   NIH MGC Project;
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Heart, and Thymus;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Heart, and Thymus;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Heart, and Thymus;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Heart, and Thymus;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Heart, and Thymus;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [9]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
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RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [10]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Heart;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC091741; AAH91741.1; -; mRNA.
DR   EMBL; BC094030; AAH94030.1; -; mRNA.
DR   EMBL; AK037928; BAC29902.1; -; mRNA.
DR   EMBL; AK084841; BAC39289.1; -; mRNA.
DR   SMR; Q58EV5; 2-84, 93-171.
DR   MGI; MGI:96113; Hmgb1.
DR   GO; GO:0005615; C:extracellular space; IDA.
DR   GO; GO:0005634; C:nucleus; TAS.
DR   GO; GO:0030235; F:nitric-oxide synthase regulator activity; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0006809; P:nitric oxide biosynthesis; IDA.
DR   GO; GO:0006810; P:transport; IDA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
SQ   SEQUENCE   215 AA;  24894 MW;  8A868DE266D552B5 CRC64;

  Query Match             99.4%;  Score 1142;  DB 2;  Length 215;
  Best Local Similarity   99.1%;  Pred. No. 1.8e-58;
  Matches  213;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              ||||||||:|||||||||||:|||||||||||||
Db        181 SKKKKEEEDDEEDEEDEEEEEEEEDEDEEEDDDDE 215


RESULT 9
HMG1_BOVIN
ID   HMG1_BOVIN     STANDARD;      PRT;   214 AA.
AC   P10103;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-AUG-1990 (Rel. 15, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   High mobility group protein 1 (HMG-1) (High mobility group protein
DE   B1).
GN   Name=HMGB1; Synonyms=HMG1;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   STRAIN=Holstein; TISSUE=Fetal thymus;
RX   MEDLINE=89057489; PubMed=3194213;
RA   Kaplan D.J., Duncan C.H.;
RT   "Full length cDNA sequence for bovine high mobility group 1 (HMG1)
RT   protein.";
RL   Nucleic Acids Res. 16:10375-10375(1988).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 115-214.
RX   MEDLINE=84128872; PubMed=6141822;
RA   Pentecost B., Dixon G.H.;
RT   "Isolation and partial sequence of bovine cDNA clones for the high-
RT   mobility-group protein (HMG-1).";
RL   Biosci. Rep. 4:49-57(1984).
RN   [3]
RP   PROTEIN SEQUENCE OF 1-37; 45-156 AND 158-194.
RX   MEDLINE=81138848; PubMed=7202717; DOI=10.1016/0014-5793(80)80453-4;
RA   Walker J.M., Gooderham K., Hastings J.R., Mayes E., Johns E.W.;
RT   "The primary structures of non-histone chromosomal proteins HMG 1 and
RT   2.";
RL   FEBS Lett. 122:264-270(1980).
RN   [4]
RP   PROTEIN SEQUENCE OF 1-36.
RX   MEDLINE=90306387; PubMed=2365081; DOI=10.1016/0014-5793(90)80308-6;
RA   Christen T., Bischoff M., Hobi R., Kuenzle C.C.;
RT   "High mobility group proteins 1 and 2 bind preferentially to
RT   brominated poly(dG-dC).poly(dG-dC) in the Z-DNA conformation but not
RT   to other types of Z-DNA.";
RL   FEBS Lett. 267:139-141(1990).
CC   -!- FUNCTION: Binds preferentially single-stranded DNA and unwinds
CC       double stranded DNA.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
CC   -!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; X12796; CAA31284.1; -; mRNA.
DR   EMBL; M26110; AAA30567.1; -; mRNA.
DR   PIR; S01947; S01947.
DR   HSSP; P07156; 1NHN.
DR   SMR; P10103; 1-83, 92-170.
DR   GO; GO:0000793; C:condensed chromosome; ISS.
DR   GO; GO:0008301; F:DNA bending activity; ISS.
DR   GO; GO:0005515; F:protein binding; ISS.
DR   GO; GO:0006288; P:base-excision repair, DNA ligation; ISS.
DR   GO; GO:0006310; P:DNA recombination; ISS.
DR   GO; GO:0006281; P:DNA repair; ISS.
DR   GO; GO:0006268; P:DNA unwinding; ISS.
DR   GO; GO:0006325; P:establishment and/or maintenance of chromat. . .; ISS.
DR   GO; GO:0017055; P:negative regulation of transcriptional prei. . .; ISS.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
KW   Chromosomal protein; Direct protein sequencing; DNA-binding;
KW   Nuclear protein; Repeat.
FT   INIT_MET      0      0
FT   DNA_BIND      8     78       HMG box 1.
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FT   DNA_BIND      94    162       HMG box 2.
FT   COMPBIAS     185    214       Asp/Glu-rich (acidic).
FT   CONFLICT      22     22       C -> S (in Ref. 3).
FT   CONFLICT     105    105       C -> A (in Ref. 3).
FT   CONFLICT     115    119       EHPGL -> PGGGV (in Ref. 2).
FT   CONFLICT     193    193       E -> D (in Ref. 3).
SQ   SEQUENCE   214 AA;  24777 MW;  B283A80FC7F0F433 CRC64;

  Query Match          99.2%;  Score 1140;  DB 1;  Length 214;
  Best Local Similarity   99.5%;  Pred. No. 2.3e-58;
  Matches  213;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
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Db           1 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 60

Qy          62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 120

Qy         122 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 180

Qy         182 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
               |||||||||||||||||||||||:||||||||
Db         181 KKKKEEEEDEEDEEDEEEEEDEEDEEEEDDDDE 214


RESULT 10
O88611_SPAEH
ID   O88611_SPAEH PRELIMINARY;      PRT;   215 AA.
AC   O88611;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   High mobility group protein.
GN   Name=HMG1;
OS   Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Spalacinae; Nannospalax.
OX   NCBI_TaxID=30637;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Lee K.-L.D., Lum H.-K., Nevo E.;
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF078817; AAC27650.2; -; Genomic_DNA.
DR   HSSP; P07156; 1NHN.
DR   SMR; O88611; 2-84, 93-171.
DR   GO; GO:0000785; C:chromatin; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
SQ   SEQUENCE   215 AA;  24905 MW;  64816B6FCF6033EA CRC64;

  Query Match          99.1%;  Score 1139;  DB 2;  Length 215;
  Best Local Similarity   99.1%;  Pred. No. 2.6e-58;
  Matches  213;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
               ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db           1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTKSAKEKGKF 60

Qy          61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy         121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy         181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
               |||||||||||||||:||||||||||||||||||
Db         181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 11
O88612_SPAEH
ID   O88612_SPAEH PRELIMINARY;      PRT;   215 AA.
AC   O88612;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   High mobility group protein.
GN   Name=HMG1;
OS   Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Spalacinae; Nannospalax.
OX   NCBI_TaxID=30637;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Lee K.-L.D., Lum H.-K., Nevo E.;
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF078818; AAC27651.1; -; Genomic_DNA.
DR   HSSP; P07156; 1NHN.
DR   SMR; O88612; 2-84, 93-171.
DR   GO; GO:0000785; C:chromatin; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
SQ   SEQUENCE   215 AA;  24923 MW;  1C6FB6845CA1E6C8 CRC64;

  Query Match          99.0%;  Score 1138;  DB 2;  Length 215;
  Best Local Similarity   98.6%;  Pred. No. 3e-58;
  Matches  212;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
               ||||||||||||||||||||||||||||||||||||||||||||||||::||||||||||
Db           1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSERCSERWKTMSAKEKGKF 60

Qy          61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy         121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||
Db         121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKEGVVKAEK 180

Qy         181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
               |||||||||||||||||||||||||||||||||||
Db         181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 12
HMG1_MOUSE
ID   HMG1_MOUSE     STANDARD;      PRT;   214 AA.
AC   P63158; P07155; P27109; P27428;
DT   01-APR-1988 (Rel. 07, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   High mobility group protein 1 (HMG-1) (High mobility group protein
DE   B1).
```

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GN   Name=Hmgb1; Synonyms=Hmg-1, Hmg1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C3H/He;
RX   MEDLINE=92335012; PubMed=1630928;
RA   Yotov W.V., St Arnaud R.;
RT   "Nucleotide sequence of a mouse cDNA encoding the nonhistone
RT   chromosomal high mobility group protein-1 (HMG1).";
RL   Nucleic Acids Res. 20:3516-3516(1992).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=94235965; PubMed=8180479; DOI=10.1007/BF00292334;
RA   Pauken C.M., Nagle D.L., Bucan M., Lo C.W.;
RT   "Molecular cloning, expression analysis, and chromosomal localization
RT   of mouse Hmg1-containing sequences.";
RL   Mamm. Genome 5:91-99(1994).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=129/Sv; TISSUE=Liver;
RX   MEDLINE=95050689; PubMed=7961836;
RA   Ferrari S., Ronfani L., Calogero S., Bianchi M.;
RT   "The mouse gene coding for high mobility group 1 protein (HMG1).";
RL   J. Biol. Chem. 269:28803-28808(1994).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=AKR/J;
RA   Ghosh B.;
RL   Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Binds preferentially single-stranded DNA and unwinds
CC       double stranded DNA. Heparin-binding protein that has a role in
CC       the extension of neurite-type cytoplasmic processes in developing
CC       cells.
CC   -!- SUBCELLULAR LOCATION: Nuclear and also cytoplasmic, associated
CC       with the plasma membrane of filipodia in process-growing cells,
CC       and also deposited into the substrate-attached material.
CC   -!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
CC   -!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; Z11997; CAA78042.1; -; mRNA.
DR   EMBL; U00431; AAA20508.1; -; mRNA.
DR   EMBL; X80457; CAA56631.1; -; Genomic_DNA.
DR   EMBL; L38477; AAA57042.1; -; mRNA.
DR   EMBL; BC006586; AAH06586.1; -; mRNA.
DR   EMBL; BC008565; AAH08565.1; -; mRNA.
DR   EMBL; BC083067; AAH83067.1; -; mRNA.
DR   EMBL; BC085090; AAH85090.1; -; mRNA.
DR   PIR; I48688; I48688.
DR   SMR; P63158; 1-83, 92-170.
DR   MGI; MGI:96113; Hmgb1.
DR   GO; GO:0005615; C:extracellular space; IDA.
DR   GO; GO:0005634; C:nucleus; TAS.
DR   GO; GO:0030235; F:nitric-oxide synthase regulator activity; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0006809; P:nitric oxide biosynthesis; IDA.
DR   GO; GO:0006810; P:transport; IDA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
KW   Chromosomal protein; DNA-binding; Heparin-binding; Nuclear protein;
KW   Repeat.
FT   INIT_MET      0      0       By similarity.
FT   DNA_BIND      8     78       HMG box 1.
FT   DNA_BIND     94    162       HMG box 2.
FT   COMPBIAS    185    214       Asp/Glu-rich (acidic).
FT   CONFLICT    178    178       E -> V (in Ref. 4).
FT   CONFLICT    189    189       D -> E (in Ref. 3).
SQ   SEQUENCE   214 AA;  24763 MW;  B3C6A91FD6F1B133 CRC64;

  Query Match             99.0%;  Score 1137;  DB 1;  Length 214;
  Best Local Similarity   99.1%;  Pred. No. 3.4e-58;
  Matches  212;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 60

Qy         62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 120

Qy        122 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 180

Qy        182 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||:|||||||||||:|||||||||||||
Db        181 KKKKEEEDDEEDEEDEEEEEEEEDEDEEEDDDDE 214


RESULT 13
HMG1_RAT
ID   HMG1_RAT       STANDARD;      PRT;   214 AA.
AC   P63159; P07155; P27109; P27428;
DT   01-APR-1988 (Rel. 07, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   High mobility group protein 1 (HMG-1) (High mobility group protein B1)
DE   (Amphoterin) (Heparin-binding protein p30).
GN   Name=Hmgb1; Synonyms=Hmg-1, Hmg1;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sprague-Dawley; TISSUE=Liver;
RX   MEDLINE=88067717; PubMed=3684582;
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RA   Paonessa G., Frank R., Cortese R.;
RT   "Nucleotide sequence of rat liver HMG1 cDNA.";
RL   Nucleic Acids Res. 15:9077-9077(1987).
RN   [2]
RP   SEQUENCE REVISION.
RA   Bianchi M.;
RL   Submitted (DEC-1988) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.
RX   MEDLINE=91358468; PubMed=1885601;
RA   Merenmies J., Pihlaskari R., Laitinen J., Wartiovaara J., Rauvala H.;
RT   "30-kDa heparin-binding protein of brain (amphoterin) involved in
RT   neurite outgrowth. Amino acid sequence and localization in the
RT   filopodia of the advancing plasma membrane.";
RL   J. Biol. Chem. 266:16722-16729(1991).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Kidney, Prostate, and Testis;
RG   NIH - Mammalian Gene Collection (MGC) project;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   PROTEIN SEQUENCE OF 1-20.
RX   MEDLINE=89066894; PubMed=2461949; DOI=10.1083/jcb.107.6.2293;
RA   Rauvala H., Merenmies J., Pihlaskari R., Korkolainen M., Huhtala M.L.,
RA   Panula P.;
RT   "The adhesive and neurite-promoting molecule p30: analysis of the
RT   amino-terminal sequence and production of antipeptide antibodies that
RT   detect p30 at the surface of neuroblastoma cells and of brain
RT   neurons.";
RL   J. Cell Biol. 107:2293-2305(1988).
RN   [6]
RP   STRUCTURE BY NMR OF 87-164.
RX   MEDLINE=93223672; PubMed=8467791;
RA   Weir H.M., Kraulis P.J., Hill C.S., Raine A.R.C., Laue E.D.,
RA   Thomas J.O.;
RT   "Structure of the HMG box motif in the B-domain of HMG1.";
RL   EMBO J. 12:1311-1319(1993).
RN   [7]
RP   STRUCTURE BY NMR OF 1-83.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=96118376; PubMed=8527432;
RA   Hardman C.H., Broadhurst R.W., Raine A.R.C., Grasser K.D.,
RA   Thomas J.O., Laue E.D.;
RT   "Structure of the A-domain of HMG1 and its interaction with DNA as
RT   studied by heteronuclear three- and four-dimensional NMR
RT   spectroscopy.";
RL   Biochemistry 34:16596-16607(1995).
CC   -!- FUNCTION: Binds preferentially single-stranded DNA and unwinds
CC       double stranded DNA. Heparin-binding protein that has a role in
CC       the extension of neurite-type cytoplasmic processes in developing
CC       cells.
CC   -!- SUBCELLULAR LOCATION: Nuclear and also cytoplasmic, associated
CC       with the plasma membrane of filipodia in process-growing cells,
CC       and also deposited into the substrate-attached material.
CC   -!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
CC   -!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; M64986; AAA40729.1; -; mRNA.
DR   EMBL; Y00463; CAA68526.1; -; mRNA.
DR   EMBL; BC061779; AAH61779.1; -; mRNA.
DR   EMBL; BC081839; AAH81839.1; -; mRNA.
DR   EMBL; BC088402; AAH88402.1; -; mRNA.
DR   PIR; A41175; NSRTH1.
DR   PDB; 1AAB; NMR; @=1-83.
DR   PDB; 1CKT; X-ray; A=7-77.
DR   PDB; 1HME; NMR; @=88-164.
DR   PDB; 1HMF; NMR; @=88-164.
DR   SMR; P63159; 1-83, 92-170.
DR   Ensembl; ENSRNOG00000030351; Rattus norvegicus.
DR   RGD; 2802; Hmgb1.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
KW   3D-structure; Chromosomal protein; Direct protein sequencing;
KW   DNA-binding; Heparin-binding; Nuclear protein; Repeat.
FT   INIT_MET      0      0
FT   DNA_BIND      8     78       HMG box 1.
FT   DNA_BIND     94    162       HMG box 2.
FT   COMPBIAS    185    214       Asp/Glu-rich (acidic).
FT   HELIX        14     29
FT   TURN         31     32
FT   HELIX        37     49
FT   TURN         50     50
FT   TURN         53     55
FT   HELIX        57     74
FT   TURN         75     76
FT   HELIX       100    115
FT   TURN        117    118
FT   HELIX       121    134
FT   HELIX       137    158
FT   TURN        159    160
SQ   SEQUENCE   214 AA;  24763 MW;  B3C6A91FD6F1B133 CRC64;

  Query Match             99.0%;  Score 1137;  DB 1;  Length 214;
  Best Local Similarity   99.1%;  Pred. No. 3.4e-58;
  Matches  212;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 60

Qy         62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 120

Qy        122 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
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Db        121 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 180

Qy        182 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||:|||||||||||:|||||||||||||
Db        181 KKKKEEEDDEEDEEDEEEEEEEEDEDEEEDDDDE 214


RESULT 14
Q6P202_MOUSE
ID   Q6P202_MOUSE PRELIMINARY;      PRT;   215 AA.
AC   Q6P202;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hmgb1 protein.
GN   Name=Hmgb1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Embryo;
RA   Strausberg R.;
RL   Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC064790; AAH64790.1; -; mRNA.
DR   HSSP; P07155; 1AAB.
DR   SMR; Q6P202; 2-84, 93-171.
DR   MGI; MGI:96113; Hmgb1.
DR   GO; GO:0005615; C:extracellular space; IDA.
DR   GO; GO:0005634; C:nucleus; TAS.
DR   GO; GO:0030235; F:nitric-oxide synthase regulator activity; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0006809; P:nitric oxide biosynthesis; IDA.
DR   GO; GO:0006810; P:transport; IDA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
SQ   SEQUENCE   215 AA;  24920 MW;  7A998DEA7AB389D8 CRC64;

  Query Match             98.9%;  Score 1136;  DB 2;  Length 215;
  Best Local Similarity   98.6%;  Pred. No. 3.9e-58;
  Matches  212;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPLAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
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Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              ||||||||:||||||||||||:||||||||||||||
Db        181 SKKKKEEEDDEEDEEDEEEEEEEEDEDEEEDDDDE 215


RESULT 15
HMG1_PIG
ID   HMG1_PIG       STANDARD;      PRT;   214 AA.
AC   P12682;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-AUG-1990 (Rel. 15, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   High mobility group protein 1 (HMG-1) (High mobility group protein
DE   B1).
GN   Name=HMGB1; Synonyms=HMG1;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC   Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=89050965; PubMed=3191113;
RA   Tsuda K.-I., Kikuchi M., Mori K., Waga S., Yoshida M.;
RT   "Primary structure of non-histone protein HMG1 revealed by the
RT   nucleotide sequence.";
RL   Biochemistry 27:6159-6163(1988).
CC   -!- FUNCTION: Binds preferentially single-stranded DNA and unwinds
CC       double stranded DNA.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
CC   -!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; M21683; AAA31050.1; -; mRNA.
DR   PIR; A28897; A28897.
DR   HSSP; P07155; 1CKT.
DR   SMR; P12682; 1-83, 92-170.
DR   GO; GO:0000793; C:condensed chromosome; ISS.
DR   GO; GO:0008301; F:DNA bending activity; ISS.
DR   GO; GO:0005515; F:protein binding; ISS.
DR   GO; GO:0006288; P:base-excision repair, DNA ligation; ISS.
DR   GO; GO:0006310; P:DNA recombination; ISS.
DR   GO; GO:0006281; P:DNA repair; ISS.
DR   GO; GO:0006268; P:DNA unwinding; ISS.
DR   GO; GO:0006325; P:establishment and/or maintenance of chromat. . .; ISS.
DR   GO; GO:0017055; P:negative regulation of transcriptional prei. . .; ISS.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
KW   Chromosomal protein; DNA-binding; Nuclear protein; Repeat.
FT   INIT_MET      0      0       By similarity.
FT   DNA_BIND      8     78       HMG box 1.
FT   DNA_BIND     94    162       HMG box 2.
FT   COMPBIAS    185    214       Asp/Glu-rich (acidic).
SQ   SEQUENCE   214 AA;  24786 MW;  B29C8A32D8D2C933 CRC64;

  Query Match             98.8%;  Score 1135;  DB 1;  Length 214;
  Best Local Similarity   99.1%;  Pred. No. 4.4e-58;
  Matches  212;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 60

Qy         62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 120

Qy        122 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
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Db        121 IGDVAKKLGEMWNNTAADDKHPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 180

Qy        182 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
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Search completed: April  6, 2006, 10:25:15
Job time : 253.898 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 10:25:39 ; Search time 61.5296 Seconds
(without alignments)
288.890 Million cell updates/sec

Title: US-10-717-984-1
Perfect score: 1149
Sequence: 1 MGKGDPKKPRGKMSSYAPFV.....DEEEEEDEEDEDEEEDDDDE 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1144	99.6	214	2	US-09-538-092-883	Sequence 883, App
2	1144	99.6	214	2	US-09-214-881A-1	Sequence 1, Appli
3	1140	99.2	214	2	US-09-214-881A-3	Sequence 3, Appli
4	1135	98.8	214	2	US-09-214-881A-4	Sequence 4, Appli
5	1128	98.2	214	2	US-09-214-881A-5	Sequence 5, Appli
6	1056.5	91.9	213	2	US-09-949-016-10813	Sequence 10813, A
7	929	80.9	320	2	US-09-949-016-10728	Sequence 10728, A
8	924	80.4	208	2	US-09-538-092-1018	Sequence 1018, Ap
9	924	80.4	208	2	US-09-214-881A-2	Sequence 2, Appli
10	921.5	80.2	209	2	US-09-214-881A-6	Sequence 6, Appli
11	915.5	79.7	209	2	US-09-214-881A-8	Sequence 8, Appli
12	900	78.3	206	2	US-09-214-881A-9	Sequence 9, Appli
13	827	72.0	208	2	US-09-214-881A-11	Sequence 11, Appl
14	824.5	71.8	879	2	US-09-914-259-38	Sequence 38, Appl
15	809.5	70.5	201	2	US-09-214-881A-10	Sequence 10, Appl
16	801	69.7	200	2	US-09-702-705-789	Sequence 789, App
17	801	69.7	200	2	US-09-736-457-789	Sequence 789, App
18	801	69.7	200	2	US-09-614-124B-789	Sequence 789, App
19	801	69.7	200	2	US-09-671-325-789	Sequence 789, App
20	801	69.7	200	2	US-09-589-184-789	Sequence 789, App
21	801	69.7	200	2	US-09-658-824-789	Sequence 789, App
22	801	69.7	200	2	US-10-017-754-789	Sequence 789, App
23	801	69.7	200	2	US-09-651-563-789	Sequence 789, App
24	801	69.7	200	2	US-09-519-642-789	Sequence 789, App
25	801	69.7	228	2	US-09-949-016-10496	Sequence 10496, A
26	796	69.3	207	2	US-09-702-705-1667	Sequence 1667, Ap
27	796	69.3	207	2	US-09-736-457-1667	Sequence 1667, Ap
28	796	69.3	207	2	US-09-614-124B-1667	Sequence 1667, Ap
29	796	69.3	207	2	US-09-671-325-1667	Sequence 1667, Ap
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32	796	69.3	207	2	US-10-017-754-1913	Sequence 1913, Ap
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34	789	68.7	200	2	US-09-702-705-324	Sequence 324, App
35	789	68.7	200	2	US-09-736-457-324	Sequence 324, App
36	789	68.7	200	2	US-09-614-124B-324	Sequence 324, App
37	789	68.7	200	2	US-09-671-325-324	Sequence 324, App
38	789	68.7	200	2	US-09-589-184-324	Sequence 324, App
39	789	68.7	200	2	US-09-658-824-324	Sequence 324, App
40	789	68.7	200	2	US-10-017-754-324	Sequence 324, App
41	789	68.7	200	2	US-09-651-563-324	Sequence 324, App
42	789	68.7	200	2	US-09-519-642-324	Sequence 324, App
43	759.5	66.1	185	2	US-09-214-881A-7	Sequence 7, Appli
44	593	51.6	110	2	US-09-513-999C-4824	Sequence 4824, Ap
45	577	50.2	110	2	US-09-513-999C-4825	Sequence 4825, Ap

ALIGNMENTS

RESULT 1
US-09-538-092-883
; Sequence 883, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 883
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P09429
US-09-538-092-883

Query Match 99.6%; Score 1144; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 2.3e-100;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 120

Qy        122 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 180

Qy        182 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
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Db        181 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 214
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RESULT 2
US-09-214-881A-1

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; Sequence 1, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
;  APPLICANT:  Ozaki, Shoichi
;  APPLICANT:  Sobajima, Junko
;  APPLICANT:  Uesugi, Hiroko
;  APPLICANT:  Okazaki, Takahiro
;  APPLICANT:  Tanaka, Masao
;  APPLICANT:  Nakao, Kazuwa
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION:  DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE:  068383.0104
;  CURRENT APPLICATION NUMBER: US/09/214,881A
;  CURRENT FILING DATE:  1999-06-07
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 214
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-214-881A-1

  Query Match             99.6%;  Score 1144;  DB 2;  Length 214;
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  Matches  214;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 60

Qy         62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
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Qy        122 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
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Db        181 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 214


RESULT 3
US-09-214-881A-3
; Sequence 3, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
;  APPLICANT:  Ozaki, Shoichi
;  APPLICANT:  Sobajima, Junko
;  APPLICANT:  Uesugi, Hiroko
;  APPLICANT:  Okazaki, Takahiro
;  APPLICANT:  Tanaka, Masao
;  APPLICANT:  Nakao, Kazuwa
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION:  DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE:  068383.0104
;  CURRENT APPLICATION NUMBER: US/09/214,881A
;  CURRENT FILING DATE:  1999-06-07
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 214
;   TYPE: PRT
;   ORGANISM: Bos taurus
US-09-214-881A-3

  Query Match             99.2%;  Score 1140;  DB 2;  Length 214;
  Best Local Similarity   99.5%;  Pred. No. 5.5e-100;
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Db          1 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 60

Qy         62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
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Db         61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 120

Qy        122 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
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Qy        182 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||
Db        181 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 214


RESULT 4
US-09-214-881A-4
; Sequence 4, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
;  APPLICANT:  Ozaki, Shoichi
;  APPLICANT:  Sobajima, Junko
;  APPLICANT:  Uesugi, Hiroko
;  APPLICANT:  Okazaki, Takahiro
;  APPLICANT:  Tanaka, Masao
;  APPLICANT:  Nakao, Kazuwa
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION:  DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE:  068383.0104
;  CURRENT APPLICATION NUMBER: US/09/214,881A
;  CURRENT FILING DATE:  1999-06-07
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 214
;   TYPE: PRT
;   ORGANISM: Sus scrofa
US-09-214-881A-4

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  Matches  212;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

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Db         61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 120

Qy        122 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
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Qy        182 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
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Db        181 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 214


RESULT 5
US-09-214-881A-5
; Sequence 5, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
;  APPLICANT:  Ozaki, Shoichi
;  APPLICANT:  Sobajima, Junko
```

```
;  APPLICANT:  Uesugi, Hiroko
;  APPLICANT:  Okazaki, Takahiro
;  APPLICANT:  Tanaka, Masao
;  APPLICANT:  Nakao, Kazuwa
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION:  DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE:  068383.0104
;  CURRENT APPLICATION NUMBER: US/09/214,881A
;  CURRENT FILING DATE:  1999-06-07
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 214
;   TYPE: PRT
;   ORGANISM: Rattus rattus
US-09-214-881A-5

  Query Match            98.2%;  Score 1128;  DB 2;  Length 214;
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  Matches  210;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

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Db          1 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 60

Qy         62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
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Db         61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 120

Qy        122 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
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Db        121 IGDVAKKLGEMWNNTAADDKHPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 180

Qy        182 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
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Db        181 KKKKEEEDDEEDEEDEEEEEEEDEEEEDDDDE 214


RESULT 6
US-09-949-016-10813
; Sequence 10813, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10813
;   LENGTH: 213
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-10813

  Query Match            91.9%;  Score 1056.5;  DB 2;  Length 213;
  Best Local Similarity  94.8%;  Pred. No. 4.2e-92;
  Matches  201;  Conservative    3;  Mismatches    7;  Indels    1;  Gaps    1;

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Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
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Db         63 EDMAKADKAHYEREMKTYIPPKGETKKKFKDPNAPKRTPSAFFLFCSAYRPKIKGEHPGL 122

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
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Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDD 212
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Db        183 SKKKKEEEEDEEDEED-EEEEDEEDEDEEDDE 213


RESULT 7
US-09-949-016-10728
; Sequence 10728, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10728
;   LENGTH: 320
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-10728

  Query Match            80.9%;  Score 929;  DB 2;  Length 320;
  Best Local Similarity  81.3%;  Pred. No. 7.7e-80;
  Matches  170;  Conservative   19;  Mismatches   20;  Indels    0;  Gaps    0;

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              |||||| |||||||||||||||||||||:||||:||||||||||||||||| ||
Db        112 MGKGDPNKPRGKMSSYAFFVQTCREEHKKKHPDSSVNFAEFSKKCSERWKTMSAKEKSKF 171

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
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Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
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Db        232 SIGDTAKKLGEMWSEQSAKDKQPYEQKAAKLKEKYEKDIAAYRAKGKSEAGKKGPGRPTG 291

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEE 209
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Db        292 SKKKNEPEDEEEEEEEEDEDEEEEDEDEE 320


RESULT 8
US-09-538-092-1018
; Sequence 1018, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
;  APPLICANT: Giot, Loic
;  APPLICANT:  Mansfield, Traci A.
;  TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
;  FILE REFERENCE: 15966-542
;  CURRENT APPLICATION NUMBER: US/09/538,092
;  CURRENT FILING DATE:  2000-03-29
;  PRIOR APPLICATION NUMBER: 60/127,352
;  PRIOR FILING DATE: 1999-04-01
;  PRIOR APPLICATION NUMBER: 60/178,965
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;  PRIOR FILING DATE: 2000-02-01
;  NUMBER OF SEQ ID NOS: 1387
;  SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1018
;   LENGTH: 208
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Polypeptide Accession Number P26583
US-09-538-092-1018

  Query Match             80.4%;  Score 924;  DB 2;  Length 208;
  Best Local Similarity   81.2%;  Pred. No. 1.4e-79;
  Matches  169;  Conservative   19;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
              ||||| |||||||||||||||||||||||||:||||:||||||||||||||||| |||
Db          1 GKGDPNKPRGKMSSYAFFVQTCREEHKKKHPDSSVNFAEFSKKCSERWKTMSAKEKSKFE 60

Qy         62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
              ||||:|||||:|||| |:|||: | | |||||||||||||||||:||||| ||||||
Db         61 DMAKSDKARYDREMKNYVPPKGDKKGKKKDPNAPKRPPSAFFLFCSEHRPKIKSEHPGLS 120

Qy        122 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
              ||| |||||||||:  :| ||||||:||||||||||||||||||| :| |||  :   |
Db        121 IGDTAKKLGEMWSEQSAKDKQPYEQKAAKLKEKYEKDIAAYRAKGKSEAGKKGPGRPTGS 180

Qy        182 KKKKEEEEDEEDEEDEEEEEDEEDEDEE 209
              ||| | |::||:||:|:|:|:|||||||
Db        181 KKKNEPEDEEEEEEEEDEDEEEEDEDEE 208


RESULT 9
US-09-214-881A-2
; Sequence 2, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
;  APPLICANT:  Ozaki, Shoichi
;  APPLICANT:  Sobajima, Junko
;  APPLICANT:  Uesugi, Hiroko
;  APPLICANT:  Okazaki, Takahiro
;  APPLICANT:  Tanaka, Masao
;  APPLICANT:  Nakao, Kazuwa
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION:  DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE:  068383.0104
;  CURRENT APPLICATION NUMBER: US/09/214,881A
;  CURRENT FILING DATE:  1999-06-07
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 208
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-214-881A-2

  Query Match             80.4%;  Score 924;  DB 2;  Length 208;
  Best Local Similarity   81.2%;  Pred. No. 1.4e-79;
  Matches  169;  Conservative   19;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
              ||||| |||||||||||||||||||||||||:||||:||||||||||||||||| |||
Db          1 GKGDPNKPRGKMSSYAFFVQTCREEHKKKHPDSSVNFAEFSKKCSERWKTMSAKEKSKFE 60

Qy         62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
              ||||:|||||:|||| |:|||: | | |||||||||||||||||:||||| ||||||
Db         61 DMAKSDKARYDREMKNYVPPKGDKKGKKKDPNAPKRPPSAFFLFCSEHRPKIKSEHPGLS 120

Qy        122 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
              ||| |||||||||:  :| ||||||:||||||||||||||||||| :| |||  :   |
Db        121 IGDTAKKLGEMWSEQSAKDKQPYEQKAAKLKEKYEKDIAAYRAKGKSEAGKKGPGRPTGS 180

Qy        182 KKKKEEEEDEEDEEDEEEEEDEEDEDEE 209
              ||| | |::||:||:|:|:|:|||||||
Db        181 KKKNEPEDEEEEEEEEDEDEEEEDEDEE 208


RESULT 10
US-09-214-881A-6
; Sequence 6, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
;  APPLICANT:  Ozaki, Shoichi
;  APPLICANT:  Sobajima, Junko
;  APPLICANT:  Uesugi, Hiroko
;  APPLICANT:  Okazaki, Takahiro
;  APPLICANT:  Tanaka, Masao
;  APPLICANT:  Nakao, Kazuwa
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION:  DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE:  068383.0104
;  CURRENT APPLICATION NUMBER: US/09/214,881A
;  CURRENT FILING DATE:  1999-06-07
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 209
;   TYPE: PRT
;   ORGANISM: Sus scrofa
US-09-214-881A-6

  Query Match             80.2%;  Score 921.5;  DB 2;  Length 209;
  Best Local Similarity   81.4%;  Pred. No. 2.3e-79;
  Matches  171;  Conservative   18;  Mismatches   20;  Indels    1;  Gaps    1;

Qy          2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
              ||||| |||||||||||||||||||||||||:||||:||||||||||||||||| |||
Db          1 GKGDPNKPRGKMSSYAFFVQTCREEHKKKHPDSSVNFAEFSKKCSERWKTMSAKEKSKFE 60

Qy         62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
              ||||:|||||:|||| |:|||: | | |||||||||||||||||:||||| ||||||
Db         61 DMAKSDKARYDREMKNYVPPKGDKKGKKKDPNAPKRPPSAFFLFCSEHRPKIKSEHPGLS 120

Qy        122 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
              ||| |||||||||:  :| ||||||:||||||||||||||||||| :| |||  :   |
Db        121 IGDTAKKLGEMWSEQSAKDKQPYEQKAAKLKEKYEKDIAAYRAKGKGEAGKKGPGRPTGS 180

Qy        182 KKKKEEEEDEEDEEDEEEEEDEEDEDEEED 211
              ||| | ||||:||:|||:||||:|||:|:
Db        181 -KKKNEPEDEEEEEEEEEDEDEEEEDEDEE 209


RESULT 11
US-09-214-881A-8
; Sequence 8, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
;  APPLICANT:  Ozaki, Shoichi
;  APPLICANT:  Sobajima, Junko
;  APPLICANT:  Uesugi, Hiroko
;  APPLICANT:  Okazaki, Takahiro
;  APPLICANT:  Tanaka, Masao
;  APPLICANT:  Nakao, Kazuwa
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION:  DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE:  068383.0104
;  CURRENT APPLICATION NUMBER: US/09/214,881A
;  CURRENT FILING DATE:  1999-06-07
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;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 209
;   TYPE: PRT
;   ORGANISM: Rattus rattus
US-09-214-881A-8

  Query Match             79.7%;  Score 915.5;  DB 2;  Length 209;
  Best Local Similarity   80.5%;  Pred. No. 8.6e-79;
  Matches  169;  Conservative   19;  Mismatches   21;  Indels    1;  Gaps    1;

Qy          2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
              ||||| |||||||||||||||||||||||||:||||:||||||||||||||||||| |||
Db          1 GKGDPNKPRGKMSSYAFPVQTCREEHKKKHPDSSVNFAEFSKKCSERWKTMSAKEKSKFE 60

Qy         62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
              ||||:|||||:|||| |:|||| | | |||||||||||||||||:||||| ||||||
Db         61 DMAKSDKARYDREMKNYVPPKGDKKGKKKDPNAPKRPPSAFFLFCSEHRPKIKSEHPGLS 120

Qy        122 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
              ||| ||||||||:  :| ||||||:||||||||||||||||||| :  |||  :   |
Db        121 IGDTAKKLGEMWSEQSAKDKQPYEQKAAKLKEKYEKDIAAYRAKGKSEVGKKGPGRPTGS 180

Qy        182 KKKKEEEEDEEDEEDEEEEEDEEDEDEEED 211
              ||| | ||||:||:||::||||:|||:|:
Db        181 -KKKNEPEDEEEEEEEEDDEDEEEEDEDEE 209


RESULT 12
US-09-214-881A-9
; Sequence 9, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
;  APPLICANT:  Ozaki, Shoichi
;  APPLICANT:  Sobajima, Junko
;  APPLICANT:  Uesugi, Hiroko
;  APPLICANT:  Okazaki, Takahiro
;  APPLICANT:  Tanaka, Masao
;  APPLICANT:  Nakao, Kazuwa
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION:  DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE:  068383.0104
;  CURRENT APPLICATION NUMBER: US/09/214,881A
;  CURRENT FILING DATE:  1999-06-07
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 206
;   TYPE: PRT
;   ORGANISM: Gallus gallus
US-09-214-881A-9

  Query Match             78.3%;  Score 900;  DB 2;  Length 206;
  Best Local Similarity   80.1%;  Pred. No. 2.5e-77;
  Matches  165;  Conservative   18;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
              ||||| |||||||||:|||||  ||||||||:||||:|||:||||||||||:|||||||
Db          1 GKGDPNKPRGKMSSYAYFVQTCPREHKKKHPDSSVNFAEFSRKCSERWKTMSSKEKGKFE 60

Qy         62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
              :||| |||||:|||| |:||||| | | |||||||||||||||||:||||| :|||||
Db         61 EMAKGDKARYDREMKNYVPPKGEKKGKKKDPNAPKRPPSAFFLFCSEHRPKIKNDHPGLS 120

Qy        122 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
              ||| ||||||||:  :| ||||||:||||||||||||||||||| | || |||  :   |
Db        121 IGDTAKKLGEMWSEQSAKDKQPYEQKAAKLKEKYEKDIAAYRAKSKSDAGKKGPGRPAGS 180

Qy        182 KKKKEEEEDEEDEEDEEEEEDEEDED 207
              ||| | ||:||:|||||||||:||||:
Db        181 KKKAEPEEEEEEEEDEEEEEEEDEE 206


RESULT 13
US-09-214-881A-11
; Sequence 11, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
;  APPLICANT:  Ozaki, Shoichi
;  APPLICANT:  Sobajima, Junko
;  APPLICANT:  Uesugi, Hiroko
;  APPLICANT:  Okazaki, Takahiro
;  APPLICANT:  Tanaka, Masao
;  APPLICANT:  Nakao, Kazuwa
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION:  DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE:  068383.0104
;  CURRENT APPLICATION NUMBER: US/09/214,881A
;  CURRENT FILING DATE:  1999-06-07
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 208
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-214-881A-11

  Query Match             72.0%;  Score 827;  DB 2;  Length 208;
  Best Local Similarity   74.0%;  Pred. No. 2e-70;
  Matches  154;  Conservative   23;  Mismatches   31;  Indels    0;  Gaps    0;

Qy          2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
              ||||| || |||||||||||||||||||::||||:| |||||:|||||||||  |||
Db          1 GKGDPIKPLGKMSSYAFFVQTCREEHKKKHPNSSVNFAEISKKCSKRWKTMSAKENSKFE 60

Qy         62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
              |:||:||| | |||| |: |||: | | |||||||||||| ||||| ||||| |:||||
Db         61 DLAKSDKACYYREMKNYVSPKGDKKGKKKDPNAPKRPPSAFCLFCSENRPKIKIEYPGLS 120

Qy        122 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
              ||| ||||||||:  :| :|||||:|||||||||| |||| ||| :| |||  :   |
Db        121 IGDTAKKLGEMWSEQSAKEKQPYEQKAAKLKEKYEKDFAAYRVKGKSEAGKKGPGRPAGS 180

Qy        182 KKKKEEEEDEEDEEDEEEEEDEEDEDEE 209
              ||| : |::||:||:|||:|: |:||||
Db        181 KKKNDSEDEEEEEEEEEEDEEGEEEDEE 208


RESULT 14
US-09-914-259-38
; Sequence 38, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
;  APPLICANT: Makowski, Lee
;  APPLICANT:  Hyman, Paul
;  APPLICANT:  Williams, Mark
;  TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
;  FILE REFERENCE: 8471-010-999
;  CURRENT APPLICATION NUMBER: US/09/914,259
;  CURRENT FILING DATE:  2000-11-21
;  NUMBER OF SEQ ID NOS: 180
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
;   LENGTH: 879
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-914-259-38

  Query Match             71.8%;  Score 824.5;  DB 2;  Length 879;
  Best Local Similarity   85.4%;  Pred. No. 1.9e-69;
  Matches  158;  Conservative    9;  Mismatches   17;  Indels    1;  Gaps    1;
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Qy          20 VQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFEDMAKADKARYEREMKTYI 79
               |  | ||||||:||||| |||| ||||| |||: ||||||||||||||| |||||||||
Db         695 VDPC-EEHKKKNPDASVKFSEFLKKCSETWKTIFAKEKGKFEDMAKADKAHYEREMKTYI 753

Qy          80 PPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAAD 139
               ||||| |||||||||||||| ||||||||||||||||||||| || |||  |||||||
Db         754 PPKGEKKKKFKDPNAPKRPPLAFFLFCSEYRPKIKGEHPGLSIDDVVKKLAGMWNNTAAA 813

Qy         140 DKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKSKKKKEEEEDEEDEEDEEE 199
               ||| |||||||||||:|||||||||||::||| |||||||||||||||||||::||
Db         814 DKQFYEKKAAKLKEKYKKDIAAYRAKGKPNSAKKRVVKAEKSKKKKEEEEDEEDEQEEEN 873

Qy         200 EEDEE 204
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Db         874 EEDDD 878


RESULT 15
US-09-214-881A-10
; Sequence 10, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
;  APPLICANT:  Ozaki, Shoichi
;  APPLICANT:  Sobajima, Junko
;  APPLICANT:  Uesugi, Hiroko
;  APPLICANT:  Okazaki, Takahiro
;  APPLICANT:  Tanaka, Masao
;  APPLICANT:  Nakao, Kazuwa
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION:  DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE:  068383.0104
;  CURRENT APPLICATION NUMBER: US/09/214,881A
;  CURRENT FILING DATE:  1999-06-07
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 201
;   TYPE: PRT
;   ORGANISM: Gallus gallus
US-09-214-881A-10

  Query Match             70.5%;  Score 809.5;  DB 2;  Length 201;
  Best Local Similarity   72.3%;  Pred. No. 8.5e-69;
  Matches  154;  Conservative   21;  Mismatches   25;  Indels   13;  Gaps    3;

Qy           3 KGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFED 62
               |||||||:||||:|||||||||||||||:|:  |||:|||||||||||||:||| ||::
Db           2 KGDPKKPKGKMSAYAFFVQTCREEHKKKNPEVPVNFAEFSKKCSERWKTMSSKEKAKFDE 61

Qy          63 MAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLSI 122
               |||||| ||:|||| | | ||  ||  |||||||||| |||||||:||||  :||:||
Db          62 MAKADKVRYDREMKDYGPAKGGKKK--KDPNAPKRPPSGFFLFCSEFRPKIKSTNPGISI 119

Qy         123 GDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKSK 182
               |||||||||||| :  :|||| ||||||||||:| |::||| | ||     | |:
Db         120 GDVAKKLGEMWNNLSDGEKQPYNNKAAKLKEKYEKDVADYKSKGKFDGAKGA---ATKAA 176

Qy         183 KKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
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Db         177 RKKVEEEDEEEEEDEEE--------EDEDDDDE 201


Search completed: April  6, 2006, 10:27:52
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 10:26:34 ; Search time 204.391 Seconds
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439.516 Million cell updates/sec

Title: US-10-717-984-1
Perfect score: 1149
Sequence: 1 MGKGDPKKPRGKMSSYAFFV.....DEEEEEDEEDEDEEEDDDDE 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1149	100.0	215	4	US-10-087-192-1446	Sequence 1446, Ap
2	1149	100.0	215	4	US-10-147-447-1	Sequence 1, Appli
3	1149	100.0	215	4	US-10-300-072-1	Sequence 1, Appli
4	1149	100.0	215	4	US-10-456-949-1	Sequence 1, Appli
5	1149	100.0	215	4	US-10-456-947-1	Sequence 1, Appli
6	1149	100.0	215	4	US-10-718-495-1	Sequence 1, Appli
7	1149	100.0	215	4	US-10-717-984-1	Sequence 1, Appli
8	1149	100.0	215	5	US-10-868-577A-63	Sequence 63, Appl
9	1149	100.0	215	5	US-10-868-549-22	Sequence 22, Appl
10	1149	100.0	215	5	US-10-938-992-74	Sequence 74, Appl
11	1145	99.7	215	5	US-10-938-992-38	Sequence 38, Appl
12	1144	99.6	214	3	US-09-214-881A-1	Sequence 1, Appli
13	1144	99.6	214	5	US-10-726-195-1	Sequence 1, Appli
14	1144	99.6	221	5	US-10-938-992-40	Sequence 40, Appl
15	1142	99.4	215	4	US-10-147-447-2	Sequence 2, Appli
16	1142	99.4	215	4	US-10-300-072-2	Sequence 2, Appli
17	1142	99.4	215	4	US-10-456-949-2	Sequence 2, Appli
18	1142	99.4	215	4	US-10-456-947-2	Sequence 2, Appli
19	1142	99.4	215	4	US-10-718-495-2	Sequence 2, Appli
20	1142	99.4	215	4	US-10-717-984-2	Sequence 2, Appli
21	1142	99.4	215	5	US-10-938-992-18	Sequence 18, Appl
22	1142	99.4	220	4	US-10-087-192-1443	Sequence 1443, Ap
23	1142	99.4	252	5	US-10-938-992-5	Sequence 5, Appli
24	1140	99.2	214	3	US-09-214-881A-3	Sequence 3, Appli
25	1140	99.2	214	5	US-10-726-195-3	Sequence 3, Appli
26	1140	99.2	215	5	US-10-938-992-37	Sequence 37, Appl
27	1135	98.8	214	3	US-09-214-881A-4	Sequence 4, Appli
28	1135	98.8	214	5	US-10-726-195-4	Sequence 4, Appli
29	1129	98.3	215	6	US-11-013-684-17	Sequence 17, Appl
30	1128	98.2	214	3	US-09-214-881A-5	Sequence 5, Appli
31	1128	98.2	214	5	US-10-726-195-5	Sequence 5, Appli
32	1122.5	97.7	216	4	US-10-147-447-18	Sequence 18, Appl
33	1122.5	97.7	216	4	US-10-300-072-18	Sequence 18, Appl
34	1122.5	97.7	216	4	US-10-300-072-24	Sequence 24, Appl
35	1122.5	97.7	216	4	US-10-456-949-18	Sequence 18, Appl
36	1122.5	97.7	216	4	US-10-456-947-6	Sequence 6, Appli
37	1122.5	97.7	216	4	US-10-456-947-10	Sequence 10, Appl
38	1122.5	97.7	216	4	US-10-718-495-18	Sequence 18, Appl
39	1122.5	97.7	216	4	US-10-718-495-24	Sequence 24, Appl
40	1122.5	97.7	216	4	US-10-717-984-18	Sequence 18, Appl
41	1122.5	97.7	216	4	US-10-717-984-24	Sequence 24, Appl
42	1122.5	97.7	216	5	US-10-938-992-1	Sequence 1, Appli
43	1061	92.3	211	4	US-10-300-072-25	Sequence 25, Appl
44	1061	92.3	211	4	US-10-456-947-12	Sequence 12, Appl
45	1061	92.3	211	4	US-10-718-495-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-10-087-192-1446
; Sequence 1446, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1446
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-192-1446

Query Match 100.0%; Score 1149; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 3.6e-70;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
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RESULT 2
US-10-147-447-1
; Sequence 1, Application US/10147447
; Publication No. US20030060410A1
; GENERAL INFORMATION:

```
;  APPLICANT: Tracey, Kevin J.
;  APPLICANT:  Yang, Huan
;  APPLICANT:  Warren Jr., Howland Shaw
;  APPLICANT:  Fink, Mitchell P.
;  TITLE OF INVENTION: Use of HMG Fragments as
;  TITLE OF INVENTION:  Anti-Inflammatory Agents
;  FILE REFERENCE: 3268.1001-001
;  CURRENT APPLICATION NUMBER: US/10/147,447
;  CURRENT FILING DATE:  2002-08-16
;  PRIOR APPLICATION NUMBER: 60/291,034
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-147-447-1

  Query Match             100.0%;  Score 1149;  DB 4;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-70;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 3
US-10-300-072-1
; Sequence 1, Application US/10300072
; Publication No. US20030144201A1
; GENERAL INFORMATION:
;  APPLICANT: Kevin J. Tracey
;  APPLICANT:  Huan Yang
;  APPLICANT:  Howland Shaw Warren, Jr.
;  APPLICANT:  Mitchell P. Fink
;  TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS ANTI-FLAMMATORY
;  TITLE OF INVENTION:  AGENTS
;  FILE REFERENCE: 3268.1001-005
;  CURRENT APPLICATION NUMBER: US/10/300,072
;  CURRENT FILING DATE:  2002-11-20
;  PRIOR APPLICATION NUMBER: US 10/147,447
;  PRIOR FILING DATE: 2002-05-15
;  PRIOR APPLICATION NUMBER: US 60/291,034
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-300-072-1

  Query Match             100.0%;  Score 1149;  DB 4;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-70;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 4
US-10-456-949-1
; Sequence 1, Application US/10456949
; Publication No. US20040005316A1
; GENERAL INFORMATION:
;  APPLICANT: Kevin J. Tracey
;  APPLICANT:  Huan Yang
;  TITLE OF INVENTION: USE OF HMG FRAGMENTS AS
;  TITLE OF INVENTION:  ANTI-INFLAMMATORY AGENTS
;  FILE REFERENCE: 3268.1001-006
;  CURRENT APPLICATION NUMBER: US/10/456,949
;  CURRENT FILING DATE:  2003-06-06
;  PRIOR APPLICATION NUMBER: 10/147,447
;  PRIOR FILING DATE: 2002-05-15
;  PRIOR APPLICATION NUMBER: 60/291,034
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-456-949-1

  Query Match             100.0%;  Score 1149;  DB 4;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-70;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 5
US-10-456-947-1
; Sequence 1, Application US/10456947
; Publication No. US20040053841A1
; GENERAL INFORMATION:
;  APPLICANT: Kevin J. Tracey
;  APPLICANT:  Huan Yang
;  TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN
;  TITLE OF INVENTION:  HMGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS
;  TITLE OF INVENTION:  ANTI-INFLAMMATORY AGENTS
;  FILE REFERENCE: 3268.1001-007
;  CURRENT APPLICATION NUMBER: US/10/456,947
;  CURRENT FILING DATE:  2003-06-06
;  PRIOR APPLICATION NUMBER: 10/147,447
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;  PRIOR FILING DATE: 2002-05-15
;  PRIOR APPLICATION NUMBER: 60/291,034
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-456-947-1

  Query Match           100.0%;  Score 1149;  DB 4;  Length 215;
  Best Local Similarity  100.0%;  Pred. No. 3.6e-70;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 6
US-10-718-495-1
; Sequence 1, Application US/10718495
; Publication No. US20040141948A1
; GENERAL INFORMATION:
;  APPLICANT: O'Keefe, Theresa L.
;  TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS
;  TITLE OF INVENTION:  ANTI-INFLAMMATORY AGENTS
;  FILE REFERENCE: 3258.1009-001
;  CURRENT APPLICATION NUMBER: US/10/718,495
;  CURRENT FILING DATE:  2003-11-12
;  PRIOR APPLICATION NUMBER: 60/427,841
;  PRIOR FILING DATE: 2002-11-20
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-718-495-1

  Query Match           100.0%;  Score 1149;  DB 4;  Length 215;
  Best Local Similarity  100.0%;  Pred. No. 3.6e-70;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 7
US-10-717-984-1
; Sequence 1, Application US/10717984
; Publication No. US20040156851A1
; GENERAL INFORMATION:
;  APPLICANT: Newman, Walter
;  TITLE OF INVENTION: HMGB1 COMBINATION THERAPIES
;  FILE REFERENCE: 3258.1008-001
;  CURRENT APPLICATION NUMBER: US/10/717,984
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,846
;  PRIOR FILING DATE: 2002-11-20
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-717-984-1

  Query Match           100.0%;  Score 1149;  DB 4;  Length 215;
  Best Local Similarity  100.0%;  Pred. No. 3.6e-70;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 8
US-10-868-577A-63
; Sequence 63, Application US/10868577A
; Publication No. US20050032697A1
; GENERAL INFORMATION:
;  APPLICANT: Alitalo et al.
;  TITLE OF INVENTION: HEPARIN BINDING VEGFR-3 LIGANDS
;  FILE REFERENCE: 28967/39359A
;  CURRENT APPLICATION NUMBER: US/10/868,577A
;  CURRENT FILING DATE:  2004-06-14
;  PRIOR APPLICATION NUMBER: US 60/478,390
;  PRIOR FILING DATE: 2003-06-12
;  PRIOR APPLICATION NUMBER: US 10/669,176
;  PRIOR FILING DATE: 2003-09-23
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-868-577A-63

  Query Match           100.0%;  Score 1149;  DB 5;  Length 215;
  Best Local Similarity  100.0%;  Pred. No. 3.6e-70;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy         121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy         181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
                |||||||||||||||||||||||||||||||||||
Db         181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 9
US-10-868-549-22
; Sequence 22, Application US/10868549
; Publication No. US20050043235A1
; GENERAL INFORMATION:
;  APPLICANT: Alitalo et al.
;  TITLE OF INVENTION: USE OF VEGF-C OR VEGF-D IN RECONSTRUCTIVE SURGERY
;  FILE REFERENCE: 28967/39117A
;  CURRENT APPLICATION NUMBER: US/10/868,549
;  CURRENT FILING DATE:  2004-06-14
;  PRIOR APPLICATION NUMBER: US 60/478,114
;  PRIOR FILING DATE: 2003-06-12
;  PRIOR APPLICATION NUMBER: US 60/478,390
;  PRIOR FILING DATE: 2003-06-12
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-868-549-22

  Query Match             100.0%;  Score 1149;  DB 5;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-70;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy          61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy         121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy         181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
                |||||||||||||||||||||||||||||||||||
Db         181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 10
US-10-938-992-74
; Sequence 74, Application US/10938992
; Publication No. US20050152903A1
; GENERAL INFORMATION:
;  APPLICANT: Newman, Walter
;  APPLICANT:  Qin, Shixin
;  APPLICANT:  O'Keefe, Theresa
;  APPLICANT:  Obar, Robert
;  TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1
;  FILE REFERENCE: 3258.1033-001
;  CURRENT APPLICATION NUMBER: US/10/938,992
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: 60/502,568
;  PRIOR FILING DATE: 2003-09-11
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 74
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-938-992-74

  Query Match             100.0%;  Score 1149;  DB 5;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-70;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy          61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy         121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy         181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
                |||||||||||||||||||||||||||||||||||
Db         181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 11
US-10-938-992-38
; Sequence 38, Application US/10938992
; Publication No. US20050152903A1
; GENERAL INFORMATION:
;  APPLICANT: Newman, Walter
;  APPLICANT:  Qin, Shixin
;  APPLICANT:  O'Keefe, Theresa
;  APPLICANT:  Obar, Robert
;  TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1
;  FILE REFERENCE: 3258.1033-001
;  CURRENT APPLICATION NUMBER: US/10/938,992
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: 60/502,568
;  PRIOR FILING DATE: 2003-09-11
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Bos taurus
US-10-938-992-38

  Query Match             99.7%;  Score 1145;  DB 5;  Length 215;
  Best Local Similarity   99.5%;  Pred. No. 6.7e-70;
  Matches  214;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
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Db           1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy          61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy         121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy         181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
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Db         181 SKKKKEEEEDEEDEEDEEEEEDEEDEEEEEDDDDE 215


RESULT 12
US-09-214-881A-1
; Sequence 1, Application US/09214881A
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; Patent No. US20020009749A1
; GENERAL INFORMATION:
;  APPLICANT:  Ozaki, Shoichi
;  APPLICANT:  Sobajima, Junko
;  APPLICANT:  Uesugi, Hiroko
;  APPLICANT:  Okazaki, Takahiro
;  APPLICANT:  Tanaka, Masao
;  APPLICANT:  Nakao, Kazuwa
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION:  DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE: 068383.0104
;  CURRENT APPLICATION NUMBER: US/09/214,881A
;  CURRENT FILING DATE:  1999-06-07
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 214
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-214-881A-1

  Query Match             99.6%;  Score 1144;  DB 3;  Length 214;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-70;
  Matches  214;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 60

Qy         62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 120

Qy        122 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 180

Qy        182 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
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Db        181 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 214


RESULT 13
US-10-726-195-1
; Sequence 1, Application US/10726195
; Publication No. US20040229279A1
; GENERAL INFORMATION:
;  APPLICANT: Ozaki, Shoichi
;  APPLICANT:  Sobajima, Junko
;  APPLICANT:  Uesugi, Hiroko
;  APPLICANT:  Okazaki, Takahiro
;  APPLICANT:  Tanaka, Masao
;  APPLICANT:  Nakao, Kazuwa
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE: 068383.0104
;  CURRENT APPLICATION NUMBER: US/10/726,195
;  CURRENT FILING DATE:  2003-12-02
;  PRIOR APPLICATION NUMBER: US/09/214,881A
;  PRIOR FILING DATE: 1999-06-07
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 214
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-726-195-1

  Query Match             99.6%;  Score 1144;  DB 5;  Length 214;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-70;
  Matches  214;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
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Db          1 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 60

Qy         62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
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Db         61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 120

Qy        122 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 180

Qy        182 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
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Db        181 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 214


RESULT 14
US-10-938-992-40
; Sequence 40, Application US/10938992
; Publication No. US20050152903A1
; GENERAL INFORMATION:
;  APPLICANT: Newman, Walter
;  APPLICANT:  Qin, Shixin
;  APPLICANT:  O'Keefe, Theresa
;  APPLICANT:  Obar, Robert
;  TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1
;  FILE REFERENCE: 3258.1033-001
;  CURRENT APPLICATION NUMBER: US/10/938,992
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: 60/502,568
;  PRIOR FILING DATE: 2003-09-11
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40
;   LENGTH: 221
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: rec-HMGB1-His6
US-10-938-992-40

  Query Match             99.6%;  Score 1144;  DB 5;  Length 221;
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  Matches  214;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 67

Qy         62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 127

Qy        122 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
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Db        128 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 187

Qy        182 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
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Db        188 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 221


RESULT 15
US-10-147-447-2
; Sequence 2, Application US/10147447
; Publication No. US20030060410A1
; GENERAL INFORMATION:
;  APPLICANT: Tracey, Kevin J.
;  APPLICANT:  Yang, Huan
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;  APPLICANT:  Warren Jr., Howland Shaw
;  APPLICANT:  Fink, Mitchell P.
;  TITLE OF INVENTION: Use of HMG Fragments as
;  TITLE OF INVENTION:  Anti-Inflammatory Agents
;  FILE REFERENCE: 3268.1001-001
;  CURRENT APPLICATION NUMBER: US/10/147,447
;  CURRENT FILING DATE:  2002-08-16
;  PRIOR APPLICATION NUMBER: 60/291,034
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-147-447-2

  Query Match             99.4%;  Score 1142;  DB 4;  Length 215;
  Best Local Similarity   99.1%;  Pred. No. 1.1e-69;
  Matches  213;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
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Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              ||||||||:|||||||||||||:|||||||||||||
Db        181 SKKKKEEEDDEEDEEDEEEEEEEEDEDEEEDDDDE 215


Search completed: April  6, 2006, 10:32:46
Job time : 204.391 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 10:28:08 ; Search time 26.875 Seconds
(without alignments)
249.536 Million cell updates/sec

Title: US-10-717-984-1
Perfect score: 1149
Sequence: 1 MGKGDPKKPRGKMSSYAFFV.....DEEEEEDEEDEDEEEDDDDE 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 184161

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /SIDS5/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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8: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1149	100.0	215	6	US-10-821-234-1443	Sequence 1443, Ap
2	1149	100.0	215	7	US-11-186-422-11	Sequence 11, Appl
3	1142	99.4	215	7	US-11-186-422-12	Sequence 12, Appl
4	824.5	71.8	879	7	US-11-169-041-192	Sequence 192, App
5	681	59.3	169	6	US-10-821-234-1234	Sequence 1234, Ap
6	370	32.2	69	7	US-11-186-422-14	Sequence 14, Appl
7	287	25.0	54	6	US-10-719-150-6	Sequence 6, Appli
8	287	25.0	54	7	US-11-186-422-13	Sequence 13, Appl
9	278.5	24.2	502	7	US-11-087-099-8879	Sequence 8879, Ap
10	273	23.8	146	7	US-11-172-740-1569	Sequence 1569, Ap
11	268	23.3	141	7	US-11-087-099-3073	Sequence 3073, Ap
12	267.5	23.3	149	7	US-11-087-099-3510	Sequence 3510, Ap
13	267.5	23.3	149	7	US-11-172-740-1571	Sequence 1571, Ap
14	267.5	23.3	160	7	US-11-087-099-1105	Sequence 1105, Ap
15	263.5	22.9	142	7	US-11-087-099-4976	Sequence 4976, Ap
16	259	22.5	154	7	US-11-087-099-2474	Sequence 2474, Ap
17	259	22.5	154	7	US-11-172-740-1570	Sequence 1570, Ap
18	253.5	22.1	372	7	US-11-087-099-6977	Sequence 6977, Ap
19	251	21.8	388	7	US-11-087-099-4330	Sequence 4330, Ap
20	250.5	21.8	145	7	US-11-172-740-1572	Sequence 1572, Ap
21	250	21.8	446	7	US-11-087-099-370	Sequence 370, App
22	248	21.6	152	7	US-11-087-099-313	Sequence 313, App
23	248	21.6	152	7	US-11-172-740-1566	Sequence 1566, Ap
24	247	21.5	141	7	US-11-087-099-9185	Sequence 9185, Ap
25	247	21.5	487	7	US-11-087-099-11126	Sequence 11126, A
26	242	21.1	152	7	US-11-172-740-1565	Sequence 1565, Ap
27	240.5	20.9	380	7	US-11-087-099-5374	Sequence 5374, Ap
28	239	20.8	187	7	US-11-096-568A-32735	Sequence 32735, A
29	239	20.8	241	7	US-11-096-568A-32734	Sequence 32734, A
30	239	20.8	257	7	US-11-096-568A-32733	Sequence 32733, A
31	233	20.3	139	7	US-11-096-568A-13611	Sequence 13611, A
32	229.5	20.0	139	7	US-11-096-568A-26884	Sequence 26884, A
33	229.5	20.0	187	7	US-11-096-568A-26883	Sequence 26883, A
34	227.5	19.8	140	7	US-11-172-740-1564	Sequence 1564, Ap
35	220	19.1	164	7	US-11-096-568A-3510	Sequence 3510, Ap
36	218.5	19.0	234	7	US-11-096-568A-21031	Sequence 21031, A
37	216.5	18.8	165	7	US-11-096-568A-21033	Sequence 21033, A
38	216.5	18.8	212	7	US-11-096-568A-21032	Sequence 21032, A
39	212.5	18.5	137	7	US-11-096-568A-3511	Sequence 3511, Ap
40	209	18.2	124	7	US-11-096-568A-9681	Sequence 9681, Ap
41	209	18.2	162	7	US-11-096-568A-9680	Sequence 9680, Ap
42	206	17.9	93	7	US-11-087-099-869	Sequence 869, App
43	205	17.8	93	7	US-11-087-099-9518	Sequence 9518, Ap
44	202.5	17.6	92	7	US-11-087-099-8838	Sequence 8838, Ap
45	202.5	17.6	487	7	US-11-124-368A-308	Sequence 308, App

ALIGNMENTS

RESULT 1
US-10-821-234-1443
; Sequence 1443, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1443
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1443

Query Match 100.0%; Score 1149; DB 6; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.7e-77;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
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Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEDEEDEDEEEDDDDE 215
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Db        181 SKKKKEEEEDEEDEEDEEEEDEEDEDEEEDDDDE 215
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RESULT 2
US-11-186-422-11
; Sequence 11, Application US/11186422
; Publication No. US20060057679A1

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; GENERAL INFORMATION:
;  APPLICANT: Critical Therapeutics, Inc.
;  APPLICANT:  O'Keefe, Theresa
;  APPLICANT:  Luciano, Peter
;  APPLICANT:  Qin, Shixin
;  TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
;  FILE REFERENCE: 3258.1021-003
;  CURRENT APPLICATION NUMBER: US/11/186,422
;  CURRENT FILING DATE:  2005-07-20
;  PRIOR APPLICATION NUMBER: 60/589,678
;  PRIOR FILING DATE: 2004-07-20
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-186-422-11

  Query Match             100.0%;  Score 1149;  DB 7;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-77;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 3
US-11-186-422-12
; Sequence 12, Application US/11186422
; Publication No. US20060057679A1
; GENERAL INFORMATION:
;  APPLICANT: Critical Therapeutics, Inc.
;  APPLICANT:  O'Keefe, Theresa
;  APPLICANT:  Luciano, Peter
;  APPLICANT:  Qin, Shixin
;  TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
;  FILE REFERENCE: 3258.1021-003
;  CURRENT APPLICATION NUMBER: US/11/186,422
;  CURRENT FILING DATE:  2005-07-20
;  PRIOR APPLICATION NUMBER: 60/589,678
;  PRIOR FILING DATE: 2004-07-20
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-11-186-422-12

  Query Match             99.4%;  Score 1142;  DB 7;  Length 215;
  Best Local Similarity   99.1%;  Pred. No. 8.8e-77;
  Matches  213;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
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Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
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Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||:|||||||||||||:|||||||||||
Db        181 SKKKKEEEDDEEDEEDEEEEEEEDEDEEEDDDDE 215


RESULT 4
US-11-169-041-192
; Sequence 192, Application US/11169041
; Publication No. US20060019284A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
;  TITLE OF INVENTION:  COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
;  TITLE OF INVENTION:  KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: 10001 NP
;  CURRENT APPLICATION NUMBER: US/11/169,041
;  CURRENT FILING DATE:  2005-06-28
;  PRIOR APPLICATION NUMBER: 60/584,405
;  PRIOR FILING DATE: 2004-06-30
;  NUMBER OF SEQ ID NOS: 527
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 192
;   LENGTH: 879
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-169-041-192

  Query Match             71.8%;  Score 824.5;  DB 7;  Length 879;
  Best Local Similarity   85.4%;  Pred. No. 6e-53;
  Matches  158;  Conservative    9;  Mismatches   17;  Indels    1;  Gaps    1;

Qy         20 VQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFEDMAKADKARYEREMKTYI 79
              |  | ||||||:||||| |||| ||||| |||: |||||||||||||||| |||||||||
Db        695 VDPC-EEHKKKNPDASVKFSEFLKKCSETWKTIFAKEKGKFEDMAKADKAHYEREMKTYI 753

Qy         80 PPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAAD 139
              ||||| |||||||||||||| ||||||||||||||||||||| || |||  |||||||
Db        754 PPKGEKKKKFKDPNAPKRPPLAFFLFCSEYRPKIKGEHPGLSIDDVVKKLAGMWNNTAAA 813

Qy        140 DKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKSKKKKEEEEDEEDEEDEEE 199
              ||| |||||||||||:|||||||||||::||| |||||||||||||||||::||
Db        814 DKQFYEKKAAKLKEKYKKDIAAYRAKGKPNSAKKRVVKAEKSKKKKEEEEDEEDEQEEEN 873

Qy        200 EEDEE 204
              |||::
Db        874 EEDDD 878


RESULT 5
US-10-821-234-1234
; Sequence 1234, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
;  APPLICANT: Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  APPLICANT:  Andarmani, Susan
;  APPLICANT:  Tang, Y. Tom
;  TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
;  FILE REFERENCE: 821A
;  CURRENT APPLICATION NUMBER: US/10/821,234
;  CURRENT FILING DATE:  2004-04-07
;  PRIOR APPLICATION NUMBER: US 60/462,047
;  PRIOR FILING DATE: 2003-04-07
;  NUMBER OF SEQ ID NOS: 1704
;  SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1234
```

```
;   LENGTH: 169
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(169)
;   OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-821-234-1234

  Query Match             59.3%;  Score 681;  DB 6;  Length 169;
  Best Local Similarity   75.1%;  Pred. No. 3.2e-43;
  Matches  127;  Conservative   13;  Mismatches   29;  Indels    0;  Gaps    0;

Qy         14 SSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFEDMAKADKARYER 73
              |||||||||||||||||||:||||:||||||||||||||||| |||||||:|||||:|
Db          1 SSYAFFVQTCREEHKKKHPDSSVNFAEFSKKCSERWKTMSAKEKSKFEDMAKSDKARYDR 60

Qy         74 EMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMW 133
              ||| |:||||: | | |||||||||||||||||:||||| ||||||||| |||| |||
Db         61 EMKNYVPPKGDKKGKKKDPNAPKRPPSAFFLFCSEHRPKIKSEHPGLSIGDTAKKLDEMW 120

Qy        134 NNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKSK 182
              :  :  ||||||::||  ||:| || |    |||  | |:|      ||
Db        121 SEQSGQDKQPYEQEAAYAKEEYGKDFAPILPKGKRXARKEGSGSPTSSK 169


RESULT 6
US-11-186-422-14
; Sequence 14, Application US/11186422
; Publication No. US20060057679A1
; GENERAL INFORMATION:
;  APPLICANT: Critical Therapeutics, Inc.
;  APPLICANT:  O'Keefe, Theresa
;  APPLICANT:  Luciano, Peter
;  APPLICANT:  Qin, Shixin
;  TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
;  FILE REFERENCE: 3258.1021-003
;  CURRENT APPLICATION NUMBER: US/11/186,422
;  CURRENT FILING DATE:  2005-07-20
;  PRIOR APPLICATION NUMBER: 60/589,678
;  PRIOR FILING DATE: 2004-07-20
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 69
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-186-422-14

  Query Match             32.2%;  Score 370;  DB 7;  Length 69;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-21;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         93 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60

Qy        153 EKYEKDIAA 161
              |||||||||
Db         61 EKYEKDIAA 69


RESULT 7
US-10-719-150-6
; Sequence 6, Application US/10719150
; Publication No. US20040120953A1
; GENERAL INFORMATION:
;  APPLICANT: Kevin J. Tracey
;  APPLICANT:  Haichao Wang
;  TITLE OF INVENTION: ANTAGONISTS OF HMG1 FOR TREATING
;  TITLE OF INVENTION:  INFLAMMATORY CONDITIONS
;  FILE REFERENCE: 3268.1000-011
;  CURRENT APPLICATION NUMBER: US/10/719,150
;  CURRENT FILING DATE:  2003-11-21
;  PRIOR APPLICATION NUMBER: US/10/300,068
;  PRIOR FILING DATE: 2002-11-20
;  PRIOR APPLICATION NUMBER: US 10/210,747
;  PRIOR FILING DATE: 2002-07-31
;  PRIOR APPLICATION NUMBER: US 09/503,632
;  PRIOR FILING DATE: 2000-02-14
;  PRIOR APPLICATION NUMBER: US 09/248,574
;  PRIOR FILING DATE: 1999-02-11
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 54
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-719-150-6

  Query Match             25.0%;  Score 287;  DB 6;  Length 54;
  Best Local Similarity   100.0%;  Pred. No. 5.7e-15;
  Matches   54;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         32 PDASVNFSEFSKKCSERWKTMSAKEKGKFEDMAKADKARYEREMKTYIPPKGET 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 PDASVNFSEFSKKCSERWKTMSAKEKGKFEDMAKADKARYEREMKTYIPPKGET 54


RESULT 8
US-11-186-422-13
; Sequence 13, Application US/11186422
; Publication No. US20060057679A1
; GENERAL INFORMATION:
;  APPLICANT: Critical Therapeutics, Inc.
;  APPLICANT:  O'Keefe, Theresa
;  APPLICANT:  Luciano, Peter
;  APPLICANT:  Qin, Shixin
;  TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
;  FILE REFERENCE: 3258.1021-003
;  CURRENT APPLICATION NUMBER: US/11/186,422
;  CURRENT FILING DATE:  2005-07-20
;  PRIOR APPLICATION NUMBER: 60/589,678
;  PRIOR FILING DATE: 2004-07-20
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 54
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-186-422-13

  Query Match             25.0%;  Score 287;  DB 7;  Length 54;
  Best Local Similarity   100.0%;  Pred. No. 5.7e-15;
  Matches   54;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         32 PDASVNFSEFSKKCSERWKTMSAKEKGKFEDMAKADKARYEREMKTYIPPKGET 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 PDASVNFSEFSKKCSERWKTMSAKEKGKFEDMAKADKARYEREMKTYIPPKGET 54


RESULT 9
US-11-087-099-8879
; Sequence 8879, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
;  CURRENT FILING DATE:  2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 8879
;   LENGTH: 502
;   TYPE: PRT
;   ORGANISM: Daucus carota
```

US-11-087-099-8879

Query Match 24.2%; Score 278.5; DB 7; Length 502;
Best Local Similarity 31.8%; Pred. No. 2.5e-13;
Matches 82; Conservative 39; Mismatches 86; Indels 51; Gaps 8;

```
Qy          1 MGKGDPKK--PRGKMSS--YAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKE 56
              :|| : ||  |  |  |  || :::    | ||::|||  | | |   : :|||::|:|
Db        161 LGKKEKKKVCPEKKKPSPPYALWLKDQWTEVKKENPDA--EFKEISTMLAAKWKTVTAEE 218

Qy         57 KGKFEDMAKADKARY----------------EREMK---------TYIPPKGETK---- 86
              |  :|:  :|:|  |                | | |          |:  | ||:
Db        219 KKPYEEKYQAEKEAYLKIVGAEKRENEAMKLLEEEQKQRTAMELLEQYMQFKEETENDKK 278

Qy         87 ---KKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQP 143
                 || |||  || | |||||| :| |  :  |    :: :| |  || | |    :| |
Db        279 KKTKKEKDPLKPKHPVSAFFLFMNERRADLVAEKK--NVLEVGKITGEEWKNMTEKEKAP 336

Qy        144 YEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKSK----------KKKEEEEDEED 193
              ||: | | | :| : :  |: |   :||     : | ||          ||||: |:
Db        337 YEEMAKKNKNQYLQQMEVYKKKKDEEAASLQKEEEELSKIQKQEAMQLLKKKEKTENLIK 396

Qy        194 EEDEEEEEDEEDEDEEED 211
              :  || :: :: | :  |
Db        397 KTKEERQKKQKGEKKIVD 414
```

RESULT 10
US-11-172-740-1569
; Sequence 1569, Application US/11172740
; Publication No. US20060057724A1
; GENERAL INFORMATION:
; APPLICANT: MASCIA, Peter
; APPLICANT: ALEXANDROV, Nickolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR
; TITLE OF INVENTION: PLANT CHARACTERISTICS AND PHENOTYPES
; FILE REFERENCE: 2750-1602PUS2
; CURRENT APPLICATION NUMBER: US/11/172,740
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,621
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/584,829
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/584,800
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 2523
; SEQ ID NO 1569
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(146)
; OTHER INFORMATION: Public GI no. 1052956
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for increasing seed/fruit yield or modifying frui
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for making ornamental plants with modified flower
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for making ornamental plants with modified leaves
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for making plants sterile and for genetic confine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for making plants with increased biomass
US-11-172-740-1569

Query Match 23.8%; Score 273; DB 7; Length 146;
Best Local Similarity 37.3%; Pred. No. 1.7e-13;
Matches 56; Conservative 31; Mismatches 53; Indels 10; Gaps 3;

```
Qy         65 KADKARYEREMKTYIPPKG----ETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHP-G 119
              |  |:: : : |  :  :|    ::||  |||| |||||||||:|  ::|   | :||
Db          2 KGGKSKAKSDNKLAVKKRGCETKKSKKSVKDPNKPKRPPSAFFVFMEDFRKTYKEKHPNN 61

Qy        120 LSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAE 179
                |:  | |  |: |       :| |:  || | |::||| : ||  |   :|| :     |
Db         62 KSVAAVGKAGGDKWKQLTDAEKAPFIAKAEKRKQEYEKSMQAYNRKQAGEAADE-----E 116

Qy        180 KSKKKKEEEEDEEDEEDEEEEEDEEDEDEE 209
              :| | : |  |:|::||   |:|::|:|:|
Db        117 ESDKSRSEVNDDEEDEDGSAEDDDDDDDDE 146
```

RESULT 11
US-11-087-099-3073
; Sequence 3073, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3073
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Canavalia gladiata
US-11-087-099-3073

Query Match 23.3%; Score 268; DB 7; Length 141;
Best Local Similarity 39.2%; Pred. No. 3.8e-13;
Matches 62; Conservative 23; Mismatches 45; Indels 28; Gaps 5;

```
Qy         65 KADKARYEREMKTYIPPKG------ETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHP 118
              |||    :  :|     ||      ::||  |||| |||||||||:| ||:| : | |||
Db          5 KADAKAADNRLKR----KGAGAGRKQSKKAAKDPNKPKRPPSAFFVFMSEFREQYKKEHP 60

Qy        119 -GLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVK 177
                |:  | |  |: | : :  :| |:  :| | ||:|:| | ||
Db         61 TNKSVAVVGKAGGDKWKSLSDAEKAPFVARAEKKKEEYDKSILAYN-------------- 106

Qy        178 AEKSKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              | : |   ||:: |:   : | ::|||||||| |||
Db        107 -RKLEGKNPSEEEKSDK--SKSEVNDEDEDEEEDQDDE 141
```

RESULT 12
US-11-087-099-3510
; Sequence 3510, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3510
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Vicia faba
US-11-087-099-3510

Query Match 23.3%; Score 267.5; DB 7; Length 149;

```
  Best Local Similarity   35.8%;  Pred. No. 4.4e-13;
  Matches   58;  Conservative   29;  Mismatches   54;  Indels   21;  Gaps    3;

Qy         58 GKFEDMAKADKARYEREMKTYIPPKGETK----KKFKDPNAPKRPPSAFFLFCSEYRPKI 113
              || :  :|  : :     |      ||  |    |: |||| |||||||||:| :::| :
Db          4 GKSKGESKKAETKLAVNKKGAAATKGGKKPAKGKEPKDPNKPKRPPSAFFVFMADFREQY 63

Qy        114 KGEHP-GLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAK 172
              | :||   |:  | |  || | : : ::| ||  :| | ||:||  : ||
Db         64 KKDHPNNKSVAAVGKACGEEWKSLSEEEKAPYVDRALKKKEEYEITLQAY---------- 113

Qy        173 KGVVKAEKSKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDD 214
                  |  : |::||  :  : |  :|||::||||::|||
Db        114 ------NKKLEGKDDEEGSDKSKSEVNDEDEDEEDEEDEDDD 149


RESULT 13
US-11-172-740-1571
; Sequence 1571, Application US/11172740
; Publication No. US20060057724A1
; GENERAL INFORMATION:
;  APPLICANT: MASCIA, Peter
;  APPLICANT:  ALEXANDROV, Nickolai
;  APPLICANT:  BROVER, Vyacheslav
;  TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR
;  TITLE OF INVENTION:  PLANT CHARACTERISTICS AND PHENOTYPES
;  FILE REFERENCE: 2750-1602PUS2
;  CURRENT APPLICATION NUMBER: US/11/172,740
;  CURRENT FILING DATE:  2005-06-30
;  PRIOR APPLICATION NUMBER: 60/583,621
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/584,829
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/584,800
;  PRIOR FILING DATE: 2004-06-30
;  NUMBER OF SEQ ID NOS: 2523
; SEQ ID NO 1571
;   LENGTH: 149
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(149)
;   OTHER INFORMATION: Public GI no. 729737
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: Utility: Useful for increasing seed/fruit yield or modifying frui
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: Utility: Useful for making ornamental plants with modified flower
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: Utility: Useful for making ornamental plants with modified leaves
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: Utility: Useful for making plants sterile and for genetic confine
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: Utility: Useful for making plants with increased biomass
US-11-172-740-1571

  Query Match             23.3%;  Score 267.5;  DB 7;  Length 149;
  Best Local Similarity   35.8%;  Pred. No. 4.4e-13;
  Matches   58;  Conservative   29;  Mismatches   54;  Indels   21;  Gaps    3;

Qy         58 GKFEDMAKADKARYEREMKTYIPPKGETK----KKFKDPNAPKRPPSAFFLFCSEYRPKI 113
              || :  :|  : :     |      ||  |    |: |||| |||||||||:| :::| :
Db          4 GKSKGESKKAETKLAVNKKGAAATKGGKKPAKGKEPKDPNKPKRPPSAFFVFMADFREQY 63

Qy        114 KGEHP-GLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAK 172
              | :||   |:  | |  || | : : ::| ||  :| | ||:||  : ||
Db         64 KKDHPNNKSVAAVGKACGEEWKSLSEEEKAPYVDRALKKKEEYEITLQAY---------- 113

Qy        173 KGVVKAEKSKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDD 214
                  |  : |::||  :  : |  :|||::||||::|||
Db        114 ------NKKLEGKDDEEGSDKSKSEVNDEDEDEEDEEDEDDD 149


RESULT 14
US-11-087-099-1105
; Sequence 1105, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
;  CURRENT FILING DATE:  2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1105
;   LENGTH: 160
;   TYPE: PRT
;   ORGANISM: Hordeum vulgare subsp. vulgare
US-11-087-099-1105

  Query Match             23.3%;  Score 267.5;  DB 7;  Length 160;
  Best Local Similarity   39.6%;  Pred. No. 4.8e-13;
  Matches   65;  Conservative   24;  Mismatches   62;  Indels   13;  Gaps    5;

Qy         54 AKEKGKFEDMAKADKARYEREMKTYIP-PKGETKKKFKDPNAPKRPPSAFFLFCSEYRPK 112
              || ||     ||||     :       |  ||:  |  |||| ||| |||||:|  |:| :
Db          4 AKSKG----AAKADTKLAVKSKGAEKPAAKGKKGKAGKDPNKPKRAPSAFFVFMGEFREE 59

Qy        113 IKGEHP-GLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAA 171
               | ::|   |:  | |  || | : :  :| |:  || ||| :| | ||:|  ||:   |
Db         60 FKQKNPKNKSVAAVGKAAGERWKSLSESEKAPFVAKANKLKGEYNKAIASYN-KGESTTA 118

Qy        172 KKGVVKAEKSKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
                  | |    || ||::|:| |: : |  :|:|:|  |: |
Db        119 ------APKKASSKEVEEEDEEESDKSKSEINDDDDDEGSDEAE 156


RESULT 15
US-11-087-099-4976
; Sequence 4976, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
;  CURRENT FILING DATE:  2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 4976
;   LENGTH: 142
;   TYPE: PRT
;   ORGANISM: Nicotiana tabacum
US-11-087-099-4976

  Query Match             22.9%;  Score 263.5;  DB 7;  Length 142;
  Best Local Similarity   38.1%;  Pred. No. 8.2e-13;
  Matches   56;  Conservative   27;  Mismatches   53;  Indels   11;  Gaps    3;

Qy         65 KADKARYEREMKTYIPPKG----ETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHP-G 119
              |  |::   : |  :  |      : ||  |||| |||||||||:|  |:|   | :||
Db          2 KGGKSKAGADSKLGVRKKATETKKAKKAAKDPNKPKRPPSAFFVFMEEFRKTYKEKHPNN 61

Qy        120 LSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAE 179
               |:  | |  |: |   :  :| ||: || | | :|:|:: ||  |   ||      : :
Db         62 KSVAAVGKAGGDAWKKLSEAEKAPYQAKAEKRKAEYQKNMDAYNRKQAGDA------EED 115
```

```
Qy        180 KSKKKKEEEEDEEDEEDEEEEEDEEDE 206
                :| | | |  |::||:|:  ||:|:|:
Db        116 ESDKSKSEVHDDDDEDDDGSEEEEDDD 142
```

Search completed: April 6, 2006, 10:33:30
Job time : 26.875 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 10:33:08 ; Search time 189 Seconds
(without alignments)
499.822 Million cell updates/sec

Title: US-10-717-984-1
Perfect score: 215
Sequence: 1 MGKGDPKKPRGKMSSYAFFV.....DEEEEEDEEDEDEEEDDDDE 215

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2442881

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	215	100.0	215	6	ABU07499	Abu07499 Protein d
2	215	100.0	215	6	AAE35859	Aae35859 Human HMG
3	215	100.0	215	7	ADD40789	Add40789 Human HMG
4	215	100.0	215	7	ADD40788	Add40788 Human HMG
5	215	100.0	215	7	ABM85677	Abm85677 Human pro
6	215	100.0	215	8	ADO60491	Ado60491 Human hig
7	215	100.0	215	8	ADO25918	Ado25918 Human hig
8	215	100.0	215	8	ADO71477	Ado71477 Human hig
9	215	100.0	215	8	ADR45922	Adr45922 Human hig
10	215	100.0	215	8	ABM81508	Abm81508 Tumour-as
11	215	100.0	215	9	ADW81011	Adw81011 Amphoteri
12	215	100.0	215	9	ADX69343	Adx69343 Human amp
13	215	100.0	215	9	ADY14248	Ady14248 PRO polyp
14	215	100.0	215	9	ADY85326	Ady85326 Human hig
15	215	100.0	215	9	ADY85085	Ady85085 Human HMG
16	215	100.0	215	9	ADZ80804	Adz80804 Amino aci
17	214	99.5	214	7	ADD47645	Add47645 Human Pro
18	214	99.5	214	7	ADE60447	Ade60447 Human Pro
19	214	99.5	214	7	ADE57980	Ade57980 Human Pro
20	214	99.5	214	7	ADE57984	Ade57984 Human Pro
21	214	99.5	214	7	ADE60732	Ade60732 Human Pro
22	214	99.5	214	7	ADE60728	Ade60728 Human Pro
23	214	99.5	214	8	ADS17580	Ads17580 Amino aci
24	214	99.5	221	9	ADY85051	Ady85051 Human HMG
25	210	97.7	229	5	ABP64829	Abp64829 Human pro
26	188	87.4	215	5	ABB57220	Abb57220 Mouse isc
27	188	87.4	215	6	AAE35860	Aae35860 Mouse and
28	188	87.4	215	7	ADD47643	Add47643 Rat Prote
29	188	87.4	215	8	ADO25919	Ado25919 Mouse/rat
30	188	87.4	215	8	ADO71478	Ado71478 Mouse/rat
31	188	87.4	215	8	ADR87104	Adr87104 High Mobi
32	188	87.4	215	9	ADY85327	Ady85327 Mouse and
33	188	87.4	220	7	ABM85676	Abm85676 Mouse pro
34	188	87.4	252	9	ADY85016	Ady85016 Human HMG
35	187	87.0	214	7	ADE60730	Ade60730 Rat Prote
36	187	87.0	214	7	ADE57978	Ade57978 Rat Prote
37	187	87.0	214	7	ADE57982	Ade57982 Rat Prote
38	187	87.0	214	7	ADE60726	Ade60726 Rat Prote
39	187	87.0	214	7	ADE60445	Ade60445 Rat Prote
40	156	72.6	178	5	ABP42191	Abp42191 Human ova
41	150	69.8	152	2	AAY73828	Aay73828 Human pro
42	147	68.4	176	6	ADA55380	Ada55380 Human pro
43	137	63.7	215	9	AEA90125	Aea90125 Human hig
44	127	59.1	168	8	ABM81641	Abm81641 Tumour-as
45	121	56.3	215	9	ADY85029	Ady85029 Rat and m

ALIGNMENTS

RESULT 1
ABU07499
ID ABU07499 standard; protein; 215 AA.
XX
AC ABU07499;
XX
DT 28-JAN-2003 (first entry)
XX
DE Protein differentially regulated in prostate cancer #102.
XX
KW Prostate cancer; gene expression; differential regulation;
KW molecular marker; drug target; cancer detection; cancer diagnosis;
KW cancer staging; cancer grading; cancer assessing; cancer monitoring.
XX
OS Homo sapiens.
XX
PN WO200281638-A2.
XX
PD 17-OCT-2002.
XX
PF 08-APR-2002; 2002WO-US010824.
XX
PR 06-APR-2001; 2001US-0281731P.
PR 06-APR-2001; 2001US-0281732P.
XX
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
XX
PI Sun Z, Jay G;
XX
DR WPI; 2003-058520/05.
DR N-PSDB; ABX10404.
XX
PT Novel genes which are differentially regulated in prostate cancer, useful
PT for diagnosing prostate cancer in prostate tissue sample and assessing
PT therapeutic or preventive intervention in prostate cancer patients.
XX
PS Claim 1; Page 413-414; 416pp; English.
XX
CC The invention describes genes (I) which are differentially regulated in
CC prostate cancer. (I) Is useful for diagnosing a prostate cancer in a
CC sample comprising prostate tissue, which involves determining the number
CC of target genes which are differentially-regulated in the sample, where
CC the number is indicative of the probability that the sample comprises
CC prostate cancer. (I) Is useful for assessing a therapeutic or preventive
CC intervention in a subject having a prostate cancer, which involves
CC determining the expression levels in a sample comprising prostate tissue
CC of target genes which are differentially-regulated in prostate cancer.

```
CC   Preferably, the expression levels of at least 10 genes are determined.
CC   (I) is also useful for identifying agents that modulate a biological
CC   activity of a polypeptide differentially-regulated in prostate cancer
CC   cells, which involves contacting a polypeptide differentially-regulated
CC   in prostate cancer cells with a test agent under conditions effective for
CC   the test agent to modulate a biological activity of the polypeptide, and
CC   determining whether the test agent modulates the biological activity. (I)
CC   is useful as molecular markers, as drug targets, and for detecting,
CC   diagnosing, staging, grading, assessing, monitoring, prognosticating,
CC   preventing or treating, determining predisposition to diseases and
CC   conditions especially relating to prostate cancer. (I) and its expression
CC   products are used in the diagnostic test to assay for presence of cancer
CC   e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in
CC   blood etc. (I) is useful for assessing cancer e.g., to determine the type
CC   of cancer, its stage of development, the nature of genetic defect, etc.
CC   The polypeptide encoded by (I) can be used as target for therapy or drug
CC   discovery. (I) can also be used for expressing the polypeptide and thus
CC   for searching specific binding partners of the polypeptide. (I) is useful
CC   in therapeutic applications to treat prostate cancer. The identification
CC   of specific genes, and groups of genes, expressed in pathways
CC   physiologically relevant to prostate cancer permits the definition of
CC   functional and disease pathways and the delineation of targets in these
CC   pathways which are useful in diagnostic, therapeutic, and clinical
CC   applications. This is the amino acid sequence of a protein diferentially
CC   regulated in prostate cancer
XX
SQ   Sequence 215 AA;

  Query Match             100.0%;  Score 215;  DB 6;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-195;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 2
AAE35859
ID   AAE35859 standard; protein; 215 AA.
XX
AC   AAE35859;
XX
DT   17-JUN-2003  (first entry)
XX
DE   Human HMG1 protein.
XX
KW   Human; high mobility group; HMG protein; HMG A box; HMG B box; asthma;
KW   inflammatory cytokine; endotoxic shock; rheumatoid arthritis; hepatitis;
KW   appendicitis; peptic ulcer; duodenal ulcer; Crohn's disease; meningitis;
KW   allergy; immune complex disease; sinusitis; bronchitis; atherosclerosis;
KW   emphysema; HIV infection; candidiasis; malaria; filariasis; myocarditis;
KW   Hodgkin's disease; neuritis; dermatitis; myocardial ischaemia; diabetes;
KW   Alzheimer's disease; Goodpasture's syndrome; graft-versus-host disease;
KW   amoebiasis; multiple sclerosis; gout; cerebral infarction; peritonitis;
KW   gene therapy; human immunodeficiency virus; HMGB1 protein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Binding-site    9. .85
FT                   /note= "DNA  binding motif (HMG1 A box)"
FT   Binding-site    89. .162
FT                   /note= "DNA  binding motif (HMG1 B box)"
XX
PN   WO200292004-A2.
XX
PD   21-NOV-2002.
XX
PF   15-MAY-2002; 2002WO-US015329.
XX
PR   15-MAY-2001; 2001US-0291034P.
XX
PA   (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (UYPI-) UNIV PITTSBURGH.
XX
PI   Tracey KJ,  Yang H,  Warren HS,  Fink MP;
XX
DR   WPI; 2003-120594/11.
XX
PT   New isolated polypeptide having a vertebrate HMG A box, useful for
PT   inhibiting a condition associated with an activated inflammatory cytokine
PT   cascade, e.g. endotoxic shock, myocardial infarction, asthma, HIV
PT   infection, malaria and diabetes.
XX
PS   Disclosure; Fig 12A; 82pp; English.
XX
CC   The invention relates to high mobility group (HMG) protein comprising DNA
CC   binding motifs termed HMG A box and HMG B box. HMG A box or a non-
CC   naturally occurring HMG A box inhibits the release of a pro-inflammatory
CC   cytokine from a vertebrate cell. The methods and compositions of the
CC   invention are useful for inhibiting a condition characterised by
CC   activation of an inflammatory cytokine cascade such as endotoxic shock,
CC   rheumatoid arthritis, appendicitis, peptic or duodenal ulcers, Crohn's
CC   disease, peritonitis, hepatitis, asthma, allergy, immune complex disease,
CC   sinusitis, bronchitis, emphysema, HIV infection, candidiasis, malaria,
CC   filariasis, amoebiasis, dermatitis, atherosclerosis, Alzheimer's disease,
CC   myocarditis, myocardial ischaemia, meningitis, multiple sclerosis, gout,
CC   cerebral infarction, neuritis, Goodpasture's syndrome, graft-versus-host
CC   disease, diabetes and Hodgkin's disease. The invention is useful in gene
CC   therapy. The present sequence is human HMG1 (also termed as HMGB1)
CC   protein
XX
SQ   Sequence 215 AA;

  Query Match             100.0%;  Score 215;  DB 6;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-195;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 3
ADD40789
ID   ADD40789 standard; protein; 215 AA.
XX
AC   ADD40789;
XX
DT   15-JAN-2004  (first entry)
```

```
XX
DE   Human HMGB1 protein #2.
XX
KW   high mobility group B protein; HMGB1; HMGB2; HMGB3; endometrial disease;
KW   contraceptive; endometrium; pregnancy; menstrual cycle irregularity;
KW   RAGE; receptor for advanced glycation end; gynaecological; cytostatic;
KW   nuclear transcription factor complex; tumour metastasis; endometriosis;
KW   polyps; hyperplasia; carcinoma.
XX
OS   Homo sapiens.
XX
PN   WO2003051383-A2.
XX
PD   26-JUN-2003.
XX
PF   19-DEC-2002; 2002WO-EP014579.
XX
PR   19-DEC-2001; 2001DE-01062556.
XX
PA   (ALCE-) ALCEDO BIOTECH GMBH.
XX
PI   Bullerdiek J;
XX
DR   WPI; 2003-505462/47.
XX
PT   Developing treatment and diagnosis of endometrial disorders, using high
PT   mobility group B proteins, or related nucleic acid or interaction
PT   partners, as targets.
XX
PS   Disclosure; SEQ ID NO 3; 43pp; German.
XX
CC   This invention describes a novel method comprising using high mobility
CC   group B proteins (HMGB) as target molecules for development or
CC   preparation of compositions (for treatment, prevention or diagnosis of
CC   endometrial diseases, or as contraceptives. The products of the invention
CC   are used in kit for characterising the status of the endometrium,
CC   especially for presence of pregnancy or irregularities in the menstrual
CC   cycle. The proteins used in the invention can be HMGB1, 2 or 3, or SP100-
CC   HMG, and the preferred interaction partner for HMGB1 is RAGE (receptor
CC   for advanced glycation end products). The products of the invention have
CC   gynaecological, contraceptive and cytostatic activity. HMGB is part of a
CC   nuclear transcription factor complex and, extracellularly, a ligand for
CC   the surface RAGE (receptor for advanced glycation end products) which is
CC   involved in tumour metastasis. The products of the invention are used to
CC   develop treatments, preventions or diagnoses of endometrial disease,
CC   particularly endometriosis or polyps, hyperplasia or carcinoma of the
CC   endometrium, also contraceptives and methods for assessing status of the
CC   endometrium, particularly for detecting pregnancy or menstrual disorders.
CC   This sequence represents the human HMGB1 protein used in the method of
CC   the invention.
XX
SQ   Sequence 215 AA;

  Query Match             100.0%;  Score 215;  DB 7;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-195;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEEEEDDDDE 215
```

```
RESULT 4
ADD40788
ID   ADD40788 standard; protein; 215 AA.
XX
AC   ADD40788;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Human HMGB1 protein.
XX
KW   high mobility group B protein; HMGB1; HMGB2; HMGB3; endometrial disease;
KW   contraceptive; endometrium; pregnancy; menstrual cycle irregularity;
KW   RAGE; receptor for advanced glycation end; gynaecological; cytostatic;
KW   nuclear transcription factor complex; tumour metastasis; endometriosis;
KW   polyps; hyperplasia; carcinoma.
XX
OS   Homo sapiens.
XX
PN   WO2003051383-A2.
XX
PD   26-JUN-2003.
XX
PF   19-DEC-2002; 2002WO-EP014579.
XX
PR   19-DEC-2001; 2001DE-01062556.
XX
PA   (ALCE-) ALCEDO BIOTECH GMBH.
XX
PI   Bullerdiek J;
XX
DR   WPI; 2003-505462/47.
DR   N-PSDB; ADD40787.
XX
PT   Developing treatment and diagnosis of endometrial disorders, using high
PT   mobility group B proteins, or related nucleic acid or interaction
PT   partners, as targets.
XX
PS   Disclosure; Fig 4; 43pp; German.
XX
CC   This invention describes a novel method comprising using high mobility
CC   group B proteins (HMGB) as target molecules for development or
CC   preparation of compositions (for treatment, prevention or diagnosis of
CC   endometrial diseases, or as contraceptives. The products of the invention
CC   are used in kit for characterising the status of the endometrium,
CC   especially for presence of pregnancy or irregularities in the menstrual
CC   cycle. The proteins used in the invention can be HMGB1, 2 or 3, or SP100-
CC   HMG, and the preferred interaction partner for HMGB1 is RAGE (receptor
CC   for advanced glycation end products). The products of the invention have
CC   gynaecological, contraceptive and cytostatic activity. HMGB is part of a
CC   nuclear transcription factor complex and, extracellularly, a ligand for
CC   the surface RAGE (receptor for advanced glycation end products) which is
CC   involved in tumour metastasis. The products of the invention are used to
CC   develop treatments, preventions or diagnoses of endometrial disease,
CC   particularly endometriosis or polyps, hyperplasia or carcinoma of the
CC   endometrium, also contraceptives and methods for assessing status of the
CC   endometrium, particularly for detecting pregnancy or menstrual disorders.
CC   This sequence represents the human HMGB1 protein used in the method of
CC   the invention.
XX
SQ   Sequence 215 AA;

  Query Match             100.0%;  Score 215;  DB 7;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-195;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
```

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Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 5
ABM85677
ID   ABM85677 standard; protein; 215 AA.
XX
AC   ABM85677;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Human protein sequence hCP43793.
XX
KW   Cytostatic; carcinoma; lymphoma; cancer; human.
XX
OS   Homo sapiens.
XX
PN   WO2003073826-A2.
XX
PD   12-SEP-2003.
XX
PF   28-FEB-2003; 2003WO-US006235.
XX
PR   01-MAR-2002; 2002US-00087192.
XX
PA   (SAGR-) SAGRES DISCOVERY.
XX
PI   Morris DW;
XX
DR   WPI; 2003-328604/31.
XX
PT   Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
PT   comprises a nucleotide sequence.
XX
PS   Claim 5; SEQ ID NO 1446; 0pp; English.
XX
CC   The present invention relates to novel DNA and protein sequences which
CC   are associated with carcinomas. The sequences are useful for: (i) for
CC   screening drug candidates; (ii) for screening of bioactive agent capable
CC   of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
CC   a bioactive agent capable of modulating the activity of CAP; (iv) for
CC   evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
CC   carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
CC   carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
CC   (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
CC   determining Carcinoma Associated (CA) gene copy number. In addition, the
CC   CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC   carcinoma including lymphoma. The present sequence is one such CAP. Note:
CC   This patent is an equivalent to basic patent US2002182586A1, for which no
CC   sequence data was published
XX
SQ   Sequence 215 AA;

  Query Match            100.0%;  Score 215;  DB 7;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-195;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 6
ADO60491
ID   ADO60491 standard; protein; 215 AA.
XX
AC   ADO60491;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Human high mobility group protein 1 (HMG1) protein SeqID2.
XX
KW   vaccine; amyloid beta 42 aggregation; amyloid beta 42 phagocytosis;
KW   microglia; high mobility group protein 1; HMG1; nootropic;
KW   neuroprotective; microglia; vaccine; Down's syndrome; amyloid angiopathy;
KW   brain amyloidosis; Alzheimer's disease; human.
XX
OS   Homo sapiens.
XX
PN   JP2004107260-A.
XX
PD   08-APR-2004.
XX
PF   18-SEP-2002; 2002JP-00272195.
XX
PR   18-SEP-2002; 2002JP-00272195.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
DR   WPI; 2004-343837/32.
DR   N-PSDB; ADO60490.
XX
PT   Vaccine for promoting amyloid beta 42 aggregation inhibitory effect
PT   and/or amyloid beta 42 phagocytosis, useful for prophylaxis and/or
PT   treatment of Alzheimer's disease or Down's syndrome, comprises high
PT   mobility group protein 1.
XX
PS   Disclosure; SEQ ID NO 2; 56pp; Japanese.
XX
CC   This invention relates to a novel vaccine for promoting amyloid beta 42
CC   aggregation inhibitory effect and/or amyloid beta 42 phagocytosis by
CC   microglia, which comprises a high mobility group protein 1 (HMG1), its
CC   partial peptide, or its salt. The invention may be useful for the
CC   production of compounds with a nootropic or neuroprotective activity
CC   acting as promoters of inhibition of amyloid beta 42 aggregation or
CC   promoters of amyloid beta 42 phagocytosis by microglia. The invention may
CC   also be useful for the production of a vaccine. The invention is useful
CC   for prophylaxis and/or treatment of Down's syndrome or amyloid angiopathy
CC   or preventing brain amyloidosis such as Alzheimer's disease. The present
CC   sequence is that of the protein encoded by the human high mobility group
CC   protein 1 (HMG1) gene which may be used during the creation of the novel
CC   vaccine of the invention.
XX
SQ   Sequence 215 AA;

  Query Match            100.0%;  Score 215;  DB 8;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-195;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
```

```
Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 7
ADO25918
ID   ADO25918 standard; protein; 215 AA.
XX
AC   ADO25918;
XX
DT   26-AUG-2004  (first entry)
XX
DE   Human high mobility group box 1 (HMG1).
XX
KW   cytostatic; gene therapy; vaccine; pharmaceutical composition;
KW   HMGB B box; high mobility group; immune response; immunostimulation;
KW   cancer; human; high mobility group box 1; HMG1; cytokine activity.
XX
OS   Homo sapiens.
XX
PN   WO2004046338-A2.
XX
PD   03-JUN-2004.
XX
PF   19-NOV-2003; 2003WO-US036975.
XX
PR   20-NOV-2002; 2002US-0427848P.
XX
PA   (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
XX
PI   Tracey KJ;
XX
DR   WPI; 2004-420625/39.
XX
PT   New pharmaceutical composition comprises a polypeptide comprising an HMGB
PT   B box or its functional variant, useful for stimulating or increasing an
PT   immune response in an individual or for treating cancer in an individual.
XX
PS   Disclosure; SEQ ID NO 1; 68pp; English.
XX
CC   The invention describes a pharmaceutical composition comprising a
CC   polypeptide comprising an HMGB (high mobility group box) B box or its
CC   functional variant to treat a disease or condition by increasing an
CC   immune response in an individual administered with the pharmaceutical
CC   composition. Also described are: an antibody attached to a polypeptide
CC   comprising an HMGB B box or its functional variant; stimulating or
CC   increasing an immune response in an individual in need of
CC   immunostimulation; and treating cancer in an individual. The composition
CC   is useful for stimulating or increasing an immune response in an
CC   individual in need of immunostimulation or for treating cancer in an
CC   individual. This is the amino acid sequence of human high mobility group
CC   box 1 (HMG1) that can be used to stimulate cytokine activity and increase
CC   immune response to assist in treating disease.
XX
SQ   Sequence 215 AA;

  Query Match             100.0%;  Score 215;  DB 8;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-195;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 8
ADO71477
ID   ADO71477 standard; protein; 215 AA.
XX
AC   ADO71477;
XX
DT   26-AUG-2004  (first entry)
XX
DE   Human high mobility group box 1 (HMGB1) protein #1.
XX
KW   Human; high mobility group box 1; HMGB1; HMGB; HMGB A box; HMGB B box;
KW   proinflammatory cytokine; weight loss; obesity; inflammation;
KW   inflammatory cytokine cascade; sepsis; allograft rejection;
KW   rheumatoid arthritis; asthma; lupus; adult respiratory distress syndrome;
KW   chronic obstructive pulmonary disease; psoriasis; pancreatitis;
KW   peritonitis; burn; myocardial ischaemia; organic ischaemia;
KW   reperfusion ischaemia; Behcet's disease; graft-versus-host disease;
KW   Crohn's disease; ulcerative colitis; multiple sclerosis; cachexia.
XX
OS   Homo sapiens.
XX
PN   WO2004046345-A2.
XX
PD   03-JUN-2004.
XX
PF   20-NOV-2003; 2003WO-US037507.
XX
PR   20-NOV-2002; 2002US-0427841P.
PR   20-NOV-2002; 2002US-0427846P.
XX
PA   (CRIT-) CRITICAL THERAPEUTICS INC.
XX
PI   Newman W,  O'keefe TL;
XX
DR   WPI; 2004-420628/39.
XX
PT   New high mobility group box proteins, useful in treating obesity, sepsis,
PT   rheumatoid arthritis, asthma, psoriasis, burns, myocardial ischemia,
PT   Behcet's disease, ulcerative colitis, multiple sclerosis, or cachexia.
XX
PS   Claim 29; SEQ ID NO 1; 113pp; English.
XX
CC   The invention relates to a polypeptide comprising a high mobility group
CC   box protein (HMGB) A or B box. The HMGB A or B box can inhibit release of
CC   a proinflammatory cytokine from a cell treated with an HMGB protein. The
CC   invention also relates to a purified preparation of antibodies that
CC   specifically bind to the HMGB B box but do not specifically bind to non-B
CC   box epitopes of HMGB, where the antibodies can inhibit release of a
CC   proinflammatory cytokine from a cell treated with HMGB, a method for
CC   effecting weight loss or treating obesity in a patient, a method of
CC   determining whether a compound inhibits inflammation, a pharmaceutical
CC   composition comprising an HMGB protein or an antibody that binds to the
CC   protein, an agent that inhibits TNF biological activity and a method of
CC   treating a condition in a patient characterised by activation of an
CC   inflammatory cytokine cascade. Effecting weight loss or treating obesity
CC   in a patient comprises administering to the patient an amount of the
CC   polypeptide. The polypeptide, antibodies, composition and methods are
CC   useful in treating obesity and conditions characterised by activation of
CC   an inflammatory cytokine cascade, e.g. sepsis, allograft rejection,
CC   rheumatoid arthritis, asthma, lupus, adult respiratory distress syndrome,
CC   chronic obstructive pulmonary disease, psoriasis, pancreatitis,
CC   peritonitis, burns, myocardial ischaemia, organic ischaemia, reperfusion
CC   ischaemia, Behcet's disease, graft-versus-host disease, Crohn's disease,
CC   ulcerative colitis, multiple sclerosis or cachexia. This sequence
```

CC represents a human HMGB1 polypeptide of the invention.
XX
SQ Sequence 215 AA;

Query Match 100.0%; Score 215; DB 8; Length 215;
Best Local Similarity 100.0%; Pred. No. 8.2e-195;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
```

RESULT 9
ADR45922
ID ADR45922 standard; protein; 215 AA.
XX
AC ADR45922;
XX
DT 21-OCT-2004 (first entry)
XX
DE Human high mobility group protein HMGB1 protein.
XX
KW antidiabetic; ophthalmological; nephropathic; antiarthritic;
KW antiinflammatory; cytostatic; gynaecological; antipsoriatic;
KW dermatological; antiviral; vasotropic; antiarteriosclerotic; antianginal;
KW cardiant; vulnerary; antiulcer; high mobility group protein; human.
XX
OS Homo sapiens.
XX
PN WO2004061456-A2.
XX
PD 22-JUL-2004.
XX
PF 05-JAN-2004; 2004WO-EP000030.
XX
PR 03-JAN-2003; 2003DE-01000023.
PR 07-MAR-2003; 2003DE-01010160.
PR 10-AUG-2003; 2003DE-01036642.
PR 08-OCT-2003; 2003DE-01046614.
XX
PA (ALCE-) ALCEDO BIOTECH GMBH.
XX
PI Bullerdiek J;
XX
DR WPI; 2004-571355/55.
DR N-PSDB; ADR45955, ADR45956.
XX
PT Use of nucleic acids encoding basic DNA-binding proteins, and their
PT translation or transcription products, for treating diseases associated
PT with e.g. angiogenesis, neovascularization or wound healing, also for
PT drug screening.
XX
PS Claim 57; SEQ ID NO 7; 161pp; German.
XX
CC The present invention relates to the use, especially in vitro, of nucleic
CC acids encoding high mobility group proteins for the following processes:
CC angiogenesis (including in a wound bed), neovascularization,
CC transmyocardial revascularization, wound healing, epithelialization and
CC healing in cases of tooth or bone implants. The sequences and their
CC encoded protein are useful for treating a very wide range of diseases:
CC (proliferative) diabetic retinopathy, diabetic nephropathy, macular
CC degeneration, arthritis, endometriosis, histiocytosis, psoriasis,
CC rosacea, eruptive or cavernous haemangioma, tumours (especially melanoma,
CC Kaposi sarcoma and basal cell carcinoma), haemorrhoids, arteriosclerosis,
CC angina pectoris, ischaemia, infarction, infertility, wounds (including
CC diabetic and other ulcers), also diseases associated with DNA damage,
CC especially xeroderma pigmentosum, 'leather skin', skin cancers and ageing
CC (including where associated with sunburn) and cardiac infarct, including
CC cosmetic treatment, especially as a sun-protection composition. Compounds
CC identified as modulators of the specified processes can also be used
CC therapeutically. The present sequence is a protein of the invention.
XX
SQ Sequence 215 AA;

Query Match 100.0%; Score 215; DB 8; Length 215;
Best Local Similarity 100.0%; Pred. No. 8.2e-195;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
```

RESULT 10
ABM81508
ID ABM81508 standard; protein; 215 AA.
XX
AC ABM81508;
XX
DT 18-NOV-2004 (first entry)
XX
DE Tumour-associated antigenic target (TAT) polypeptide PRO71096, SEQ:3888.
XX
KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2004030615-A2.
XX
PD 15-APR-2004.
XX
PF 29-SEP-2003; 2003WO-US028547.
XX
PR 02-OCT-2002; 2002US-0414971P.
XX
PA (GETH) GENENTECH INC.
XX
PI Wu TD, Zhang Z, Zhou Y;
XX
DR WPI; 2004-347921/32.
DR N-PSDB; ACN39623.
XX
PT New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or

PT prostate cancer or tumor.
XX
PS Claim 12; SEQ ID NO 3888; 7273pp; English.
XX
CC The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT polypeptide of the invention
XX
SQ Sequence 215 AA;

Query Match 100.0%; Score 215; DB 8; Length 215;
Best Local Similarity 100.0%; Pred. No. 8.2e-195;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
```

RESULT 11
ADW81011
ID ADW81011 standard; protein; 215 AA.
XX
AC ADW81011;
XX
DT 21-APR-2005 (first entry)
XX
DE Amphoterin protein sequence.
XX
KW Vascular endothelial growth factor; VEGF;
KW vascular endothelial growth factor receptor; VEGFR; dermatological;
KW edema; gene therapy; vulnerary; injury; burn; skin cancer; cytostatic;
KW wound healing; hematoma; pain; necrosis; ischemia; vasotropic;
KW angiogenesis stimulation; vascularization; tissue regeneration;
KW amphoterin.
XX
OS Homo sapiens.
XX
PN WO2005011722-A2.
XX
PD 10-FEB-2005.
XX
PF 14-JUN-2004; 2004WO-US019197.
XX
PR 12-JUN-2003; 2003US-0478114P.
PR 12-JUN-2003; 2003US-0478390P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
XX
PI Alitalo K, Saaristo A, Karkkainen M, Tammela T, Asko-Seljavaara S;
PI Yla-Herttuala S, He Y;
XX
DR WPI; 2005-142834/15.
XX
PT Improving healing of skin graft or skin flap to underlying tissue useful
PT in mastopexy, cosmetic surgery, abdominoplasty, involves using
PT composition of vascular endothelial growth factor-C or D polynucleotides
PT and/or polypeptides.
XX
PS Example 11; SEQ ID NO 22; 119pp; English.
XX
CC The present invention relates to new vascular endothelial growth factor
CC (VEGF) proteins useful for skin healing of a skin graft onto underlying
CC tissue. The method involves contacting a skin graft/flap or underlying
CC tissue with an agent chosen from vascular endothelial growth factor C
CC (VEGF-C) polynucleotides, VEGF-C polypeptides, VEGF-D polynucleotides,
CC and VEGF-D polypeptides, in amount effective to reduce edema or increase
CC perfusion at skin graft or flap. The composition comprises a gene therapy
CC vector that encodes VEGF-C polynucleotide. The VEGF-C polypeptide
CC comprises the formula X-B-Z or Z-B-X, where X binds VEGF receptor-3
CC (VEGFR-3) and comprises a VEGFR-3 ligand amino acid sequence chosen from
CC a prepro-VEGF-C sequence, and fragments that binds VEGFR-3, where Z
CC comprises a heparin-binding amino acid sequence, and B comprises a
CC covalent attachment linking X to Z. The VEGF-C polynucleotides, VEGF-C
CC polypeptides, VEGF-D polynucleotides, and VEGF-D polypeptides comprise a
CC VEGF homology domain (VHD) and a heparin-binding domain. Vulnerary. Gene
CC therapy. The method is useful in treating skin injury such as burns or
CC skin cancer, skin grafts, cosmetic surgery, a liposuction procedure, or
CC in reconstructive surgery. The reconstructive surgery is breast
CC reconstruction following mastectomy or injury. The subject is diabetic.
CC The method is useful for improving post-surgical wound healing after
CC reconstructive and cosmetic surgery and improves complications resulting
CC from surgery which includes excessive bleeding, such as hematomas,
CC bruising and wound-healing difficulties, pain, edema, necrosis and
CC ischemia. The present sequence is amphoterin protein, which contains a
CC heparin binding domain related to the invention.
XX
SQ Sequence 215 AA;

Query Match 100.0%; Score 215; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 8.2e-195;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
```

RESULT 12
ADX69343
ID ADX69343 standard; protein; 215 AA.
XX
AC ADX69343;
XX

```
DT   05-MAY-2005  (first entry)
XX
DE   Human amphoterin.
XX
KW   amphoterin; Heparin binding protein; Neuroprotective; Nootropic;
KW   Antiparkinsonian; Anticonvulsant; VEGF-3 receptor;
KW   Angiogenesis stimulator; Gene Therapy;
KW   vascular endothelial growth factor receptor 3; VEGFR-3;
KW   angiogenesis disorder; neurodegenerative disorder; Alzheimers disease;
KW   Parkinsons disease; motor neurone disease; dementia; paralysis; VEGF-C;
KW   neurological disease; Huntingtons chorea;
KW   vascular endothelial growth factor receptor 3; neurological disease.
XX
OS   Homo sapiens.
XX
PN   WO2005016963-A2.
XX
PD   24-FEB-2005.
XX
PF   14-JUN-2004; 2004WO-US019122.
XX
PR   12-JUN-2003; 2003US-0478114P.
PR   12-JUN-2003; 2003US-0478390P.
PR   23-SEP-2003; 2003US-00669176.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
PA   (LICN ) LICENTIA LTD.
XX
PI   Alitalo K,  He Y,  Tammela T;
XX
DR   WPI; 2005-182331/19.
XX
PT   New heparin-binding Vascular Endothelial Growth Factor Receptor 3 ligands
PT   comprising prepro-VEGF-C, prepro-VEGF-D sequences or fragments, for
PT   treating neurodegenerative disorder, e.g. Alzheimer's, Parkinson's, or
PT   Huntington's disease.
XX
PS   Disclosure; SEQ ID NO 63; 219pp; English.
XX
CC   The invention relates to heparin-binding vascular endothelial growth
CC   factor receptor 3 (VEGFR-3) proteins and encoding polynucleotides. The
CC   heparin binding VEGFR-3 proteins are used for stimulating
CC   lymphangiogenesis or angiogenesis in a mammal, and for modulating the
CC   growth of mammalian endothelial cells, mammalian endothelial precursor
CC   cells or hematopoietic progenitor cells. The polypeptide may also be used
CC   for promoting recruitment, proliferation, differentiation, migration or
CC   survival of neuronal cells or neuronal precursor cells, and for treating
CC   neurodegenerative disorder, e.g. Alzheimer's diseases, Parkinson's
CC   disease, Huntington's disease, motor neuron disease, Amyotrophic Lateral
CC   Sclerosis (ALS), dementia, or cerebral palsy. The present sequence
CC   represents human amphoterin.
XX
SQ   Sequence 215 AA;

  Query Match            100.0%;  Score 215;  DB 9;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-195;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
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Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
```

```
RESULT 13
ADY14248
ID   ADY14248 standard; protein; 215 AA.
XX
AC   ADY14248;
XX
DT   05-MAY-2005  (first entry)
XX
DE   PRO polypeptide SEQ ID NO 54.
XX
KW   Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
KW   Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;
KW   Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;
KW   Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
KW   Antiallergic; ds; gene; diagnosis.
XX
OS   Homo sapiens.
XX
PN   WO2005016962-A2.
XX
PD   24-FEB-2005.
XX
PF   11-AUG-2004; 2004WO-US026249.
XX
PR   11-AUG-2003; 2003US-0493546P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Abbas A,  Clark H,  Ouyang W,  Williams MP,  Wood WI,  Wu TD;
XX
DR   WPI; 2005-182330/19.
XX
PT   New nucleic acid encoding PRO polypeptide, useful for diagnosing and
PT   treating an immune related disorder, e.g. systemic lupus erythematosus,
PT   rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
XX
PS   Claim 8; SEQ ID NO 54; 158pp; English.
XX
CC   The invention relates to an isolated nucleic acid encoding a PRO
CC   polypeptide. The polypeptide, agonist or an antagonist, antibody,
CC   composition, and method are useful for diagnosing and treating an immune
CC   related disorder, e.g. systemic lupus erythematosus, rheumatoid
CC   arthritis. The present sequence represents a DNA encoding a PRO
CC   polypeptide.
XX
SQ   Sequence 215 AA;

  Query Match            100.0%;  Score 215;  DB 9;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-195;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
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```
RESULT 14
ADY85326
ID   ADY85326 standard; protein; 215 AA.
```

```
XX
AC   ADY85326;
XX
DT   02-JUN-2005  (first entry)
XX
DE   Human high mobility group box protein HMGB1.
XX
KW   High mobility group box; HMGB1; immune disorder; infection;
KW   immunosuppressive; autoimmune disease; allergy; antiallergic;
KW   ulcerative colitis; antiinflammatory; antiulcer; gastrointestinal-gen.;
KW   Crohns disease; inflammation; asthma; antiasthmatic;
KW   rheumatoid arthritis; antirheumatic; antiarthritic; psoriasis;
KW   antipsoriatic; systemic lupus erythematosus; dermatological; antiulcer.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          32. .85
FT                   /label= A_box
FT   Region          93. .161
FT                   /label= B_box
XX
PN   WO2005025604-A2.
XX
PD   24-MAR-2005.
XX
PF   10-SEP-2004; 2004WO-US029540.
XX
PR   10-SEP-2003; 2003US-0502349P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
XX
PI   Warren HS,  Tracey KJ;
XX
DR   WPI; 2005-233421/24.
XX
PT   Treating an immune pathology in an individual comprises administering an
PT   amount of a high mobility group box (HMGB) polypeptide comprising a
PT   vertebrate or a non-naturally occurring HMGB A or B box, or its
PT   immunosuppressive fragment.
XX
PS   Claim 6; SEQ ID NO 1; 57pp; English.
XX
CC   The invention is based on the discovery that high mobility group box
CC   protein 1 (HMGB1, also known as high mobility group-1 or HMG1), when
CC   administered with an antigen, diminishes the antibody response to the
CC   administered antigen. HMGB1 has 2 DNA binding motifs, termed the A and B
CC   boxes. A claimed method of treating an immune pathology in an individual
CC   comprises administering a HMGB polypeptide comprising a vertebrate HMGB A
CC   box, a non-naturally-occurring HMGB A box, or an immunosuppressive
CC   fragment of the vertebrate or non-natural HMGB A box. The immune
CC   pathology is induced by the administration of a non-human antigen, non-
CC   self material (e.g. a cell or tissue such as bone marrow cells) or
CC   adjuvant to the individual, by the transplantation of an organ into the
CC   individual, or by infection from a microorganism. Claimed methods of
CC   protecting a subject against an immune pathology, inhibiting an immune
CC   pathology in an individual or decreasing an immune response to an
CC   administered non-human antigen comprise administering a HMGB polypeptide
CC   comprising a vertebrate HMGB A box, a non-naturally-occurring HMGB A box,
CC   or an immunosuppressive fragment of the vertebrate or non-natural A box.
CC   A claimed method of treating an autoimmune disorder in an individual
CC   comprises administering a HMGB polypeptide comprising a vertebrate HMGB A
CC   box, a non-naturally-occurring HMGB A box, or an immunosuppressive
CC   fragment of these, and a vertebrate or non-naturally-occurring HMGB B
CC   box. The HMGB polypeptide is preferably a HMGB1 peptide and may be
CC   truncated at the C-terminus. The autoimmune disease is allergy,
CC   ulcerative colitis, Crohn's disease, asthma, rheumatoid arthritis,
CC   psoriasis or systemic lupus erythematosus (all claimed). The present
CC   sequence is that of the human HMGB1 protein, which can be used as the
CC   HMGB polypeptide in methods of the invention.
XX
SQ   Sequence 215 AA;
```

```
  Query Match           100.0%;  Score 215;  DB 9;  Length 215;
  Best Local Similarity  100.0%;  Pred. No. 8.2e-195;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
```

```
RESULT 15
ADY85085
ID   ADY85085 standard; protein; 215 AA.
XX
AC   ADY85085;
XX
DT   16-JUN-2005  (first entry)
XX
DE   Human HMGB1 A box.
XX
KW   High mobility group box; HMGB1; monoclonal antibody; antibody therapy;
KW   sepsis; antibacterial immunosuppressive; graft rejection; arthritis;
KW   antiarthritic; asthma; antiasthmatic; lupus erythematosus;
KW   antiinflammatory; inflammation; dermatological;
KW   respiratory distress syndrome; respiratory-gen.; psoriasis;
KW   antipsoriatic; chronic obstructive pulmonary disease; pancreatitis;
KW   peritonitis; burns; vulnerary; ischemia; vasotropic; Behcets disease;
KW   graft versus host disease; inflammatory bowel disease;
KW   gastrointestinal-gen.; multiple sclerosis neuroprotective; cachexia;
KW   anabolic; infection; musculoskeletal disease; immune disorder.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Rattus sp.
XX
PN   WO2005026209-A2.
XX
PD   24-MAR-2005.
XX
PF   10-SEP-2004; 2004WO-US029527.
XX
PR   11-SEP-2003; 2003US-0502568P.
XX
PA   (CRIT-) CRITICAL THERAPEUTICS INC.
XX
PI   Newman W,  Qin S,  Okeefe T,  Obar R;
XX
DR   WPI; 2005-233483/24.
XX
PT   New antibody or its antigen-binding fragment specific to a vertebrate
PT   high mobility group box (HMGB) A box that inhibits release of a
PT   proinflammatory cytokine from a cell treated with HMGB protein, useful
PT   for treating, e.g. sepsis.
XX
PS   Disclosure; SEQ ID NO 2; 123pp; English.
XX
CC   The invention provides antibodies, or their antigen-binding fragments,
CC   that bind to a vertebrate high mobility group box (HMGB) polypeptide, to
CC   methods of detecting and/or identifying an agent that binds to an HMGB
CC   polypeptide, methods of treating a condition in a subject characterized
CC   by activation of an inflammatory cytokine cascade, and methods of
```

CC detecting an HMGB polypeptide in a sample. The antibody (or antigen-
CC binding fragment) binds to a vertebrate HMGB A box but does not
CC specifically bind to non-A box epitopes of HMGB, and inhibits release of
CC a proinflammatory cytokine from a vertebrate cell treated with an HMGB
CC protein. A method of treating a condition characterized by activation of
CC an inflammatory cytokine cascade comprises administering an antibody of
CC the invention, or its antigen-binding fragment. The condition is selected
CC from sepsis, allograft rejection, arthritis, asthma, lupus, adult
CC respiratory distress syndrome, chronic obstructive pulmonary disease,
CC psoriasis, pancreatitis, peritonitis, burns, ischemia, Behcet's disease,
CC graft versus host disease, inflammatory bowel disease, multiple sclerosis
CC and cachexia, especially sepsis, arthritis, or lupus. The present
CC sequence is that of the A box of human HMGB1 ADY85012. An identical
CC sequence is also found in rat and mouse HMGB1.
XX
SQ Sequence 215 AA;

Query Match 100.0%; Score 215; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 8.2e-195;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
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Search completed: April 6, 2006, 10:36:45
Job time : 189 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 10:37:03 ; Search time 41 Seconds
(without alignments)
504.551 Million cell updates/sec

Title: US-10-717-984-1
Perfect score: 215
Sequence: 1 MGKGDPKKPRGKMSSYAPFV.....DEEEEEDEEDEDEEEDDDDE 215

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 1

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	215	100.0	215	2	S02826	nonhistone chromos
2	206	95.8	215	1	S01947	nonhistone chromos
3	188	87.4	215	1	NSRTH1	nonhistone chromos
4	188	87.4	215	2	I48688	non-histone chromo
5	143	66.5	170	2	A27853	nonhistone chromos
6	141	65.6	215	2	A28897	nonhistone chromos
7	108	50.2	216	2	S29857	nonhistone chromos
8	29	13.5	172	2	A24019	nonhistone chromos
9	29	13.5	204	2	S48708	high-mobility-grou
10	29	13.5	204	2	T01071	high mobility grou
11	26	12.1	209	1	NSHUH2	nonhistone chromos
12	26	12.1	210	2	A34719	nonhistone chromos
13	26	12.1	210	2	S54774	high mobility grou
14	24	11.2	54	2	S68823	HMG1 protein homol
15	22	10.2	205	2	S26062	nonhistone chromos
16	20	9.3	210	2	S62355	high mobility grou
17	19	8.8	186	2	S30221	nonhistone chromos
18	19	8.8	207	2	JC1129	nonhistone chromos
19	19	8.8	207	2	JC1114	high-mobility grou
20	17	7.9	186	2	B61611	nonhistone chromos
21	17	7.9	792	2	T42963	hypothetical prote
22	15	7.0	201	2	I50254	HMG-1 - chicken
23	15	7.0	202	2	S22359	nonhistone chromos
24	15	7.0	215	2	I51067	gene HMG-T2 protei
25	15	7.0	387	2	S02708	troponin T - fruit
26	15	7.0	393	2	JC6179	dorsal switch prot
27	15	7.0	393	2	S50068	nonhistone chromos
28	15	7.0	396	2	S13251	troponin T - fruit
29	14	6.5	49	2	D61510	high mobility grou
30	13	6.0	207	2	B71446	hypothetical prote
31	12	5.6	447	2	T46146	hypothetical prote
32	12	5.6	571	2	S37913	hypothetical prote
33	12	5.6	599	2	S67495	huntingtin-associa
34	12	5.6	629	2	S67492	huntingtin-associa
35	12	5.6	677	2	S15667	transcription fact
36	12	5.6	798	2	T33022	hypothetical prote
37	11	5.1	238	2	S58253	hypothetical prote
38	11	5.1	240	2	S52590	SNF7 protein - yea
39	11	5.1	396	2	I50707	Sox11 transcriptio
40	11	5.1	435	2	S69035	hypothetical prote
41	11	5.1	482	2	G96616	hypothetical prote
42	11	5.1	589	2	T52070	RNA1 protein homol
43	11	5.1	589	2	A36983	RNA1 homolog fug1
44	11	5.1	713	2	A27441	nucleolin - Chines
45	11	5.1	754	2	A56619	female sterile hom

ALIGNMENTS

RESULT 1
S02826
nonhistone chromosomal protein HMG-1 - human
C;Species: Homo sapiens (man)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C;Accession: S02826; A33178; G33178
R;Wen, L.; Huang, J.K.; Johnson, B.H.; Reeck, G.R.
Nucleic Acids Res. 17, 1197-1214, 1989
A;Title: A human placental cDNA clone that encodes nonhistone chromosomal protein HMG-1.
A;Reference number: S02826; MUID:89160247; PMID:2922262
A;Accession: S02826
A;Molecule type: mRNA
A;Residues: 1-215 <WEN>
A;Cross-references: UNIPROT:P09429; UNIPARC:UPI00000015ED; EMBL:X12597; NID:g32326; PIDN
R;Ward, L.D.; Hong, J.; Whitehead, R.H.; Simpson, R.J.
Electrophoresis 11, 883-891, 1990
A;Title: Development of a database of amino acid sequences for human colon carcinoma pro
A;Reference number: A33178; MUID:91176935; PMID:2079031
A;Accession: A33178
A;Molecule type: protein
A;Residues: 2-13,'XXF' <WAR>
A;Cross-references: UNIPARC:UPI00001771D7
A;Accession: G33178
A;Molecule type: protein
A;Residues: 2-13,'XX',16-22 <WA2>
A;Cross-references: UNIPARC:UPI00001771D7
C;Genetics:
A;Gene: GDB:HMG1
A;Cross-references: GDB:133789; OMIM:163905
A;Map position: 13q12-13q12
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

Query Match 100.0%; Score 215; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 1e-179;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MGKGDPKKPRGKMSSYAPFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAPFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
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                    ||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 2
S01947
nonhistone chromosomal protein HMG-1 - bovine
N;Alternate names: 33K protein; high-mobility-group protein HMG-1
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1989 #sequence_revision 22-Apr-1995 #text_change 09-Jul-2004
C;Accession: S01947; A61611; S10959; I45910
R;Kaplan, D.J.; Duncan, C.H.
Nucleic Acids Res. 16, 10375, 1988
A;Title: Full length cDNA sequence for bovine high mobility group 1 (HMG1) protein.
A;Reference number: S01947; MUID:89057489; PMID:3194213
A;Accession: S01947
A;Molecule type: mRNA
A;Residues: 1-215 <KAP>
A;Cross-references: UNIPROT:P10103; UNIPARC:UPI000016C31D; EMBL:X12796; NID:g416; PIDN:C
R;Walker, J.M.; Gooderham, K.; Hastings, J.R.B.; Mayes, E.; Johns, E.W.
FEBS Lett. 122, 264-270, 1980
A;Title: The primary structures of non-histone chromosomal proteins HMG 1 and 2.
A;Reference number: A61611; MUID:81138848; PMID:7202717
A;Accession: A61611
A;Molecule type: protein
A;Residues: 2-22,'S',24-40;48-105,'A',107-157,'X',160-193,'D',195 <WAL>
A;Cross-references: UNIPARC:UPI0000173987; UNIPARC:UPI0000173988
R;Christen, T.; Bischoff, M.; Hobi, R.; Kuenzle, C.C.
FEBS Lett. 267, 139-141, 1990
A;Title: High mobility group proteins 1 and 2 bind preferentially to brominated poly(dG-
A;Reference number: S10726; MUID:90306387; PMID:2365081
A;Accession: S10959
A;Molecule type: protein
A;Residues: 2-22,'X',24-38 <CHR>
A;Cross-references: UNIPARC:UPI0000173989
R;Pentecost, B.T.; Dixon, G.H.
Biosci. Rep. 4, 49-57, 1984
A;Title: Isolation and partial sequence of bovine cDNA clones for the high-mobility-grou
A;Reference number: I45910; MUID:84128872; PMID:6141822
A;Accession: I45910
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 'PGG',119,'V',121-215 <PEN>
A;Cross-references: UNIPARC:UPI000016C31E; GB:M26110; NID:g163156; PIDN:AAA30567.1; PID:
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; duplication; nucleus
F;2-215/Product: nonhistone chromosomal protein HMG-1 #status predicted <MAT>
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

  Query Match             95.8%;  Score 206;  DB 1;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-172;
  Matches  206;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDE 206
              ||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDE 206


RESULT 3
NSRTH1
```

```
nonhistone chromosomal protein HMG-1 - rat
N;Alternate names: 30K heparin-binding protein, brain; amphoterin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A41175; A27298; A30188; B48771; A48771; C48771
R;Merenmies, J.; Pihlaskari, R.; Laitinen, J.; Wartiovaara, J.; Rauvala, H.
J. Biol. Chem. 266, 16722-16729, 1991
A;Title: 30-kDa heparin-binding protein of brain (amphoterin) involved in neurite outgro
A;Reference number: A41175; MUID:91358468; PMID:1885601
A;Accession: A41175
A;Molecule type: mRNA
A;Residues: 1-215 <MER>
A;Cross-references: UNIPROT:P07155; UNIPARC:UPI00000008A6; GB:M64986; NID:g202884; PIDN:
A;Note: part of this sequence, including the amino end of the mature protein, was confir
A;Note: the authors used antibodies to synthetic peptides to demonstrate this protein in
h-mobility group proteins
R;Paonessa, G.; Frank, R.; Cortese, R.
Nucleic Acids Res. 15, 9077, 1987
A;Title: Nucleotide sequence of rat liver HMG1 cDNA.
A;Reference number: A27298; MUID:88067717; PMID:3684582
A;Accession: A27298
A;Molecule type: mRNA
A;Residues: 1-10,'R',12-82,84-95,97,'AS',100-215 <PAO>
A;Cross-references: UNIPARC:UPI0000173984
R;Rauvala, H.; Merenmies, J.; Pihlaskari, R.; Korkolainen, M.; Huhtala, M.L.; Panula, P.
J. Cell Biol. 107, 2293-2305, 1988
A;Title: The adhesive and neurite-promoting molecule p30: analysis of the amino-terminal
 brain neurons.
A;Reference number: A30188; MUID:89066894; PMID:2461949
A;Accession: A30188
A;Molecule type: protein
A;Residues: 2-14,'X',16-21 <RAU>
A;Cross-references: UNIPARC:UPI0000173985
R;Parkkinen, J.; Raulo, E.; Merenmies, J.; Nolo, R.; Kajander, E.O.; Baumann, M.; Rauvala
J. Biol. Chem. 268, 19726-19738, 1993
A;Title: Amphoterin, the 30-kDa protein in a family of HMG1-type polypeptides. Enhanced
A;Reference number: A48771; MUID:93374971; PMID:8366113
A;Accession: B48771
A;Status: preliminary
A;Molecule type: protein
A;Residues: 98-105,'X',107-112 <PA2>
A;Cross-references: UNIPARC:UPI0000173986
A;Experimental source: postnatal brain
A;Note: sequence extracted from NCBI backbone (NCBIP:137788)
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;2-215/Product: nonhistone chromosomal protein HMG-1 #status experimental <MAT>
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

  Query Match             87.4%;  Score 188;  DB 1;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-156;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEE 188
              ||||||||
Db        181 SKKKKEEE 188


RESULT 4
I48688
```

non-histone chromosomal high-mobility group 1 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48688; A55402; I57021
R;Yotov, W.V.; St-Arnaud, R.
Nucleic Acids Res. 20, 3516, 1992
A;Title: Nucleotide sequence of a mouse cDNA encoding the nonhistone chromosomal high mo
A;Reference number: I48687; MUID:92335012; PMID:1630928
A;Accession: I48688
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-215 <RES>
A;Cross-references: UNIPROT:P07155; UNIPARC:UPI00000008A6; EMBL:Z11997; NID:g53381; PIDN
R;Ferrari, S.; Ronfani, L.; Calogero, S.; Bianchi, M.E.
J. Biol. Chem. 269, 28803-28808, 1994
A;Title: The mouse gene coding for high mobility group 1 protein (HMG1).
A;Reference number: A55402; MUID:95050689; PMID:7961836
A;Accession: A55402
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-189,'E',191-215 <FER>
A;Cross-references: UNIPARC:UPI000016CDD6; EMBL:X80457; NID:g620097; PIDN:CAA56631.1; PI
R;Pauken, C.M.; Nagle, D.L.; Bucan, M.; Lo, C.W.
Mamm. Genome 5, 91-99, 1994
A;Title: Molecular cloning, expression analysis, and chromosomal localization of mouse H
A;Reference number: I57021; MUID:94235965; PMID:8180479
A;Accession: I57021
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-215 <RE2>
A;Cross-references: UNIPARC:UPI00000008A6; EMBL:U00431; NID:g437101; PIDN:AAA20508.1; PI
C;Genetics:
A;Gene: hmg1
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

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  Query Match             87.4%;  Score 188;  DB 2;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-156;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEE 188
              ||||||||
Db        181 SKKKKEEE 188
```

RESULT 5
A27853
nonhistone chromosomal protein HMG-1 - Chinese hamster (fragment)
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: A27853
R;Lee, K.L.D.; Pentecost, B.T.; D'Anna, J.A.; Tobey, R.A.; Gurley, L.R.; Dixon, G.H.
Nucleic Acids Res. 15, 5051-5068, 1987
A;Title: Characterization of cDNA sequences corresponding to three distinct HMG-1 mRNA s
A;Reference number: A27853; MUID:87259986; PMID:3601666
A;Accession: A27853
A;Molecule type: mRNA
A;Residues: 1-170 <LEE>
A;Cross-references: UNIPROT:P07156; UNIPARC:UPI00001771D5
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;1-38/Domain: HMG box homology (fragment) <HMG1>
F;47-121/Domain: HMG box homology <HMG2>

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  Query Match             66.5%;  Score 143;  DB 2;  Length 170;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-117;
  Matches  143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         46 SERWKTMSAKEKGKFEDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLF 105
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 SERWKTMSAKEKGKFEDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLF 60

Qy        106 CSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAK 165
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAK 120

Qy        166 GKPDAAKKGVVKAEKSKKKKEEE 188
              |||||||||||||||||||||||
Db        121 GKPDAAKKGVVKAEKSKKKKEEE 143
```

RESULT 6
A28897
nonhistone chromosomal protein HMG-1 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: A28897
R;Tsuda, K.; Kikuchi, M.; Mori, K.; Waga, S.; Yoshida, M.
Biochemistry 27, 6159-6163, 1988
A;Title: Primary structure of non-histone protein HMG1 revealed by the nucleotide sequen
A;Reference number: A28897; MUID:89050965; PMID:3191113
A;Accession: A28897
A;Molecule type: mRNA
A;Residues: 1-215 <TSU>
A;Cross-references: UNIPROT:P12682; UNIPARC:UPI000016C6C4; GB:M21683; GB:M21684; NID:g16
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

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  Query Match             65.6%;  Score 141;  DB 2;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-115;
  Matches  141;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDK 141
              |||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDK 141
```

RESULT 7
S29857
nonhistone chromosomal protein HMG-1 - human
C;Species: Homo sapiens (man)
C;Date: 08-Dec-1993 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C;Accession: S29857
R;Stros, M.; Dixon, G.H.
Biochim. Biophys. Acta 1172, 231-235, 1993
A;Title: A retropseudogene for non-histone chromosomal protein HMG-1.
A;Reference number: S29857; MUID:93176821; PMID:8439568
A;Accession: S29857
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-216 <STR>
A;Cross-references: UNIPARC:UPI000011DFAA; EMBL:L08048; NID:g184250; PIDN:AAA64970.1; PI

```
A;Note: the authors did not translate the codon for residue 1
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

  Query Match            50.2%;  Score 108;  DB 2;  Length 216;
  Best Local Similarity  100.0%;  Pred. No. 1.5e-86;
  Matches  108;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         99 PSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKD 158
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 PSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKD 158

Qy        159 IAAYRAKGKPDAAKKGVVKAEKSKKKKEEEDEEDEEDEEEEEDEEDE 206
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        159 IAAYRAKGKPDAAKKGVVKAEKSKKKKEEEDEEDEEDEEEEEDEEDE 206


RESULT 8
A24019
nonhistone chromosomal protein HMG-T - trout (fragment)
N;Alternate names: HMG-T
C;Species: Salmo sp. (trout)
C;Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 09-Jul-2004
C;Accession: A24019
R;Pentecost, B.T.; Wright, J.M.; Dixon, G.H.
Nucleic Acids Res. 13, 4871-4888, 1985
A;Title: Isolation and sequence of cDNA clones coding for a member of the family of high
A;Reference number: A24019; MUID:85269614; PMID:4022777
A;Accession: A24019
A;Molecule type: mRNA
A;Residues: 1-172 <PEN>
A;Cross-references: UNIPROT:P07746; UNIPARC:UPI00001771D6
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;1-50/Domain: HMG box homology (fragment) <HMG1>
F;59-133/Domain: HMG box homology <HMG2>

  Query Match            13.5%;  Score 29;  DB 2;  Length 172;
  Best Local Similarity  100.0%;  Pred. No. 7.1e-18;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         34 ASVNFSEFSKKCSERWKTMSAKEKGKFED 62
              |||||||||||||||||||||||||||||
Db          1 ASVNFSEFSKKCSERWKTMSAKEKGKFED 29


RESULT 9
S48708
high-mobility-group-1 protein - trout
C;Species: Salmo sp. (trout)
C;Date: 01-Aug-1995 #sequence_revision 19-Apr-1996 #text_change 07-May-1999
C;Accession: S48708
R;Stros, M.; Nishikawa, S.; Dixon, G.H.
Eur. J. Biochem. 225, 581-591, 1994
A;Title: cDNA sequence and structure of a gene encoding trout testis high-mobility-group
A;Reference number: S48708; MUID:95045507; PMID:7957172
A;Accession: S48708
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-204 <STR>
A;Cross-references: UNIPARC:UPI00001771D9
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
F;5-82/Domain: HMG box homology <HMG1>
F;91-165/Domain: HMG box homology <HMG2>

  Query Match            13.5%;  Score 29;  DB 2;  Length 204;
  Best Local Similarity  100.0%;  Pred. No. 8.2e-18;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         34 ASVNFSEFSKKCSERWKTMSAKEKGKFED 62
              |||||||||||||||||||||||||||||
Db         33 ASVNFSEFSKKCSERWKTMSAKEKGKFED 61


RESULT 10
T01071
high mobility group protein T - rainbow trout
N;Alternate names: HMG-T protein
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01071
R;Pentecost, B.T.; Wright, J.M.; Dixon, G.H.
Nucleic Acids Res. 13, 4871-4888, 1985
A;Title: Isolation and sequence of cDNA clones coding for a member of the family of high
A;Reference number: A24019; MUID:85269614; PMID:4022777
A;Accession: T01071
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-204 <PEN>
A;Cross-references: UNIPROT:P07746; UNIPARC:UPI000012CA3E; EMBL:X02666; NID:g64327; PIDN
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
F;91-165/Domain: HMG box homology <HMG>

  Query Match            13.5%;  Score 29;  DB 2;  Length 204;
  Best Local Similarity  100.0%;  Pred. No. 8.2e-18;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         34 ASVNFSEFSKKCSERWKTMSAKEKGKFED 62
              |||||||||||||||||||||||||||||
Db         33 ASVNFSEFSKKCSERWKTMSAKEKGKFED 61


RESULT 11
NSHUH2
nonhistone chromosomal protein HMG-2 - human
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: A42425; S20061; S18068
R;Shirakawa, H.; Yoshida, M.
J. Biol. Chem. 267, 6641-6645, 1992
A;Title: Structure of a gene coding for human HMG2 protein.
A;Reference number: A42425; MUID:92202209; PMID:1551873
A;Accession: A42425
A;Molecule type: DNA
A;Residues: 2-209 <SHI>
A;Cross-references: UNIPROT:P26583; UNIPARC:UPI000012CA25; GB:M83665; NID:g184235; PIDN:A
A;Note: sequence extracted from NCBI backbone (NCBIN:89899, NCBIP:89900)
A;Note: initiator Met not shown
R;Majumdar, A.; Brown, D.; Kerby, S.; Rudzinski, I.; Polte, T.; Randhawa, Z.; Seidman, M
Nucleic Acids Res. 19, 6643, 1991
A;Title: Sequence of human HMG2 cDNA.
A;Reference number: S20061; MUID:92093633; PMID:1754403
A;Accession: S20061
A;Molecule type: mRNA
A;Residues: 1-209 <MAJ>
A;Cross-references: UNIPARC:UPI000013E34D; EMBL:X62534; NID:g32332; PIDN:CAA44395.1; PID
C;Genetics:
A;Gene: GDB:NHCP2
A;Cross-references: GDB:119451; OMIM:118880
A;Map position: 7pter-7qter
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

  Query Match            12.1%;  Score 26;  DB 1;  Length 209;
  Best Local Similarity  100.0%;  Pred. No. 3.4e-15;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 KPRGKMSSYAFFVQTCREEHKKKHPD 33
              |||||||||||||||||||||||||
Db          8 KPRGKMSSYAFFVQTCREEHKKKHPD 33
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```
RESULT 12
A34719
nonhistone chromosomal protein HMG-2 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 09-Jul-2004
C;Accession: A34719
R;Shirakawa, H.; Tsuda, K.; Yoshida, M.
Biochemistry 29, 4419-4423, 1990
A;Title: Primary structure of non-histone chromosomal protein HMG2 revealed by the nucle
A;Reference number: A34719; MUID:90275208; PMID:2350545
A;Accession: A34719
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-210 <SHI>
A;Cross-references: UNIPROT:P17741; UNIPARC:UPI000016C6C5; GB:J02895; NID:g164491; PIDN:
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

  Query Match             12.1%;  Score 26;  DB 2;  Length 210;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-15;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 KPRGKMSSYAFFVQTCREEHKKKHPD 33
              |||||||||||||||||||||||||
Db          8 KPRGKMSSYAFFVQTCREEHKKKHPD 33


RESULT 13
S54774
high mobility group 2 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S54774; S52211
R;Zwilling, S.; Koenig, H.; Wirth, T.
EMBO J. 14, 1198-1208, 1995
A;Title: High mobility group protein 2 functionally interacts with the POU domains of oc
A;Reference number: S54774; MUID:95237201; PMID:7720710
A;Accession: S54774
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-210 <ZWI>
A;Cross-references: UNIPROT:P30681; UNIPARC:UPI000016432C; EMBL:Z46757; NID:g609168; PID
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

  Query Match             12.1%;  Score 26;  DB 2;  Length 210;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-15;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 KPRGKMSSYAFFVQTCREEHKKKHPD 33
              |||||||||||||||||||||||||
Db          8 KPRGKMSSYAFFVQTCREEHKKKHPD 33


RESULT 14
S68823
HMG1 protein homolog, 6K - mouse
C;Species: Mus musculus (house mouse)
C;Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 02-Jul-1998
C;Accession: S68823
R;Sparatore, B.; Melloni, E.; Patrone, M.; Passalacqua, M.; Pontremoli, S.
FEBS Lett. 386, 95-98, 1996
A;Title: A 6 kDa protein homologous to the N-terminus of the HMG1 protein promoting stim
A;Reference number: S68823; MUID:96228042; PMID:8647297
A;Accession: S68823
A;Molecule type: mRNA
A;Residues: 1-54 <SPA>
A;Cross-references: UNIPARC:UPI00001771DD
A;Experimental source: C44 MEL cells
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
F;6-54/Domain: HMG box homology #status atypical <HMG>

  Query Match             11.2%;  Score 24;  DB 2;  Length 54;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-14;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         28 KKKHPDASVNFSEFSKKCSERWKT 51
              ||||||||||||||||||||||||
Db         28 KKKHPDASVNFSEFSKKCSERWKT 51


RESULT 15
S26062
nonhistone chromosomal protein HMG-2 - mouse
N;Alternate names: high mobility group 2 protein
C;Species: Mus musculus (house mouse)
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
C;Accession: S26062; S25487; I48408
R;Stolzenburg, F.; Dinkl, E.; Grummt, F.
Nucleic Acids Res. 20, 4927, 1992
A;Title: Nucleotide sequence of a mouse cDNA encoding the non-histone chromosomal high m
A;Reference number: I48408; MUID:93027215; PMID:1408807
A;Accession: S26062
A;Molecule type: mRNA
A;Residues: 1-205 <STO>
A;Cross-references: UNIPROT:P30681; UNIPARC:UPI000016CDD8; EMBL:X67668; NID:g51338; PIDN
A;Note: this is a revision to the sequence from reference S25487
R;Stolzenburg, F.; Dinkl, E.; Grummt, F.
submitted to the EMBL Data Library, August 1992
A;Reference number: S25487
A;Accession: S25487
A;Molecule type: mRNA
A;Residues: 1-183,'KNDSED',190-195,'E',197-198,'ED',201-202,'G',204-205,'EDEE' <STW>
A;Cross-references: UNIPARC:UPI00001771D1; EMBL:X67668
A;Note: this sequence has been revised in reference S26062
C;Genetics:
A;Gene: hmg2
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

  Query Match             10.2%;  Score 22;  DB 2;  Length 205;
  Best Local Similarity   100.0%;  Pred. No. 1e-11;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 GKMSSYAFFVQTCREEHKKKHP 32
              ||||||||||||||||||||||
Db         11 GKMSSYAFFVQTCREEHKKKHP 32


Search completed: April  6, 2006, 10:41:29
Job time : 42 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 10:33:48 ; Search time 231 Seconds
(without alignments)
656.661 Million cell updates/sec

Title: US-10-717-984-1
Perfect score: 215
Sequence: 1 MGKGDPKKPRGKMSSYAFFV.....DEEEEEDEEDEDEEEDDDDE 215

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	215	100.0	215	2	Q5T7C3_HUMAN	Q5t7c3 homo sapien
2	215	100.0	215	2	Q4R844_MACFA	Q4r844 macaca fasc
3	214	99.5	214	1	HMG1_CANFA	Q6yka4 canis famil
4	214	99.5	214	1	HMG1_HUMAN	P09429 homo sapien
5	205	95.3	214	1	HMG1_BOVIN	P10103 bos taurus
6	192	89.3	192	2	Q5T7C5_HUMAN	Q5t7c5 homo sapien
7	189	87.9	215	2	Q9QWY6_SPAEH	Q9qwy6 spalax leuc
8	188	87.4	215	2	Q548R9_RAT	Q548r9 rattus norv
9	188	87.4	215	2	Q58EV5_MOUSE	Q58ev5 m high mobi
10	187	87.0	214	1	HMG1_MOUSE	P63158 mus musculu
11	187	87.0	214	1	HMG1_RAT	P63159 rattus norv
12	181	84.2	181	2	Q8BNM0_MOUSE	Q8bnm0 mus musculu
13	178	82.8	178	2	Q8C7C4_MOUSE	Q8c7c4 mus musculu
14	160	74.4	215	2	Q9QX40_SPAEH	Q9qx40 spalax leuc
15	157	73.0	157	2	Q5T7C2_HUMAN	Q5t7c2 homo sapien
16	157	73.0	158	2	Q5T7C4_HUMAN	Q5t7c4 homo sapien
17	157	73.0	176	2	Q59GW1_HUMAN	Q59gw1 homo sapien
18	153	71.2	180	1	HMG1_CRIGR	P07156 cricetulus
19	146	67.9	162	2	Q5T7C6_HUMAN	Q5t7c6 homo sapien
20	143	66.5	215	2	O88611_SPAEH	O88611 spalax leuc
21	140	65.1	214	1	HMG1_PIG	P12682 sus scrofa
22	137	63.7	215	2	Q14321_HUMAN	Q14321 homo sapien
23	132	61.4	132	2	Q5T7C1_HUMAN	Q5t7c1 homo sapien
24	128	59.5	215	2	O88612_SPAEH	O88612 spalax leuc
25	99	46.0	215	2	Q6P202_MOUSE	Q6p202 mus musculu
26	97	45.1	97	2	Q5T7C0_HUMAN	Q5t7c0 homo sapien
27	97	45.1	215	2	Q8BQ02_MOUSE	Q8bq02 mus musculu
28	92	42.8	211	1	HMG1X_HUMAN	Q9ugv6 homo sapien
29	92	42.8	234	2	Q7TPK9_RAT	Q7tpk9 rattus norv
30	58	27.0	214	2	Q9PUK9_CHICK	Q9puk9 gallus gall
31	58	27.0	215	2	Q9YH06_CHICK	Q9yh06 gallus gall
32	54	25.1	206	2	Q5BKQ1_MOUSE	Q5bkq1 mus musculu
33	50	23.3	50	2	Q9NYD7_HUMAN	Q9nyd7 homo sapien
34	39	18.1	211	2	Q6P4N5_XENTR	Q6p4n5 xenopus tro
35	39	18.1	211	2	Q7SZ42_XENLA	Q7sz42 xenopus lae
36	37	17.2	208	2	Q80YZ1_MOUSE	Q80yz1 mus musculu
37	35	16.3	211	2	Q9NQJ4_HUMAN	Q9nqj4 homo sapien
38	31	14.4	38	1	HMG2_BOVIN	P40673 bos taurus
39	30	14.0	55	2	Q7TPS2_MOUSE	Q7tps2 mus musculu
40	30	14.0	205	2	Q6NX86_BRARE	Q6nx86 brachydanio
41	30	14.0	205	2	Q7ZVC6_BRARE	Q7zvc6 brachydanio
42	29	13.5	204	1	HMGT_ONCMY	P07746 oncorhynchu
43	27	12.6	191	2	Q75MM1_HUMAN	Q75mm1 homo sapien
44	26	12.1	190	2	Q9CT19_MOUSE	Q9ct19 mus musculu
45	26	12.1	195	2	Q96J53_HUMAN	Q96j53 homo sapien

ALIGNMENTS

RESULT 1
Q5T7C3_HUMAN
ID Q5T7C3_HUMAN PRELIMINARY; PRT; 215 AA.
AC Q5T7C3;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE High-mobility group box 1.
GN Name=HMGB1; ORFNames=RP11-550P23.1-004;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Pelan S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AL353648; CAI15600.1; -; Genomic_DNA.
DR GO; GO:0000785; C:chromatin; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
SQ SEQUENCE 215 AA; 24894 MW; 8A868CF277D417B5 CRC64;

Query Match 100.0%; Score 215; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.2e-184;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
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RESULT 2
Q4R844_MACFA
ID Q4R844_MACFA PRELIMINARY; PRT; 215 AA.
AC Q4R844;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Testis cDNA clone: QtsA-13487, similar to human high-mobility group

```
DE   box 1 (HMGB1),.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   International consortium for macaque cDNA sequencing, analysis;
RT   "DNA sequences of macaque genes expressed in brain or testis and its
RT   evolutionary implications.";
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
RA   Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.;
RT   "Substitution rate and structural divergence of 5'UTR evolution:
RT   Comparative analysis between human and cynomolgus monkey cDNAs.";
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB168615; BAE00728.1; -; mRNA.
SQ   SEQUENCE   215 AA;  24894 MW;  8A868CF277D417B5 CRC64;

  Query Match             100.0%;  Score 215;  DB 2;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-184;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 3
HMG1_CANFA
ID   HMG1_CANFA     STANDARD;      PRT;   214 AA.
AC   Q6YKA4;
DT   10-MAY-2005 (Rel. 47, Created)
DT   10-MAY-2005 (Rel. 47, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   High mobility group protein 1 (HMG-1) (High mobility group protein
DE   B1).
GN   Name=HMGB1;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC   Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA].
RX   MEDLINE=22932580; PubMed=14571134; DOI=10.1159/000073415;
RA   Murua Escobar H., Meyer B., Richter A., Becker K., Flohr A.M.,
RA   Bullerdiek J., Nolte I.;
RT   "Molecular characterization of the canine HMGB1.";
RL   Cytogenet. Genome Res. 101:33-38(2003).
CC   -!- FUNCTION: Binds preferentially single-stranded DNA and unwinds
CC       double stranded DNA (By similarity).
CC   -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC   -!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
CC   -!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AY135519; AAN11296.1; -; mRNA.
DR   EMBL; AY135521; AAN11319.1; -; Genomic_DNA.
DR   HSSP; P07155; 1AAB.
DR   SMR; Q6YKA4; 1-83, 92-170.
DR   Ensembl; ENSCAFG00000006597; Canis familiaris.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
KW   Chromosomal protein; DNA-binding; Nuclear protein; Repeat.
FT   INIT_MET      0      0       By similarity.
FT   DNA_BIND      8     78       HMG box 1.
FT   DNA_BIND     94    162       HMG box 2.
FT   COMPBIAS    185    214       Asp/Glu-rich (acidic).
SQ   SEQUENCE   214 AA;  24763 MW;  B3C6A80FC7F0F433 CRC64;

  Query Match             99.5%;  Score 214;  DB 1;  Length 214;
  Best Local Similarity   100.0%;  Pred. No. 9.7e-184;
  Matches  214;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 60

Qy         62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 120

Qy        122 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 180

Qy        182 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||
Db        181 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 214


RESULT 4
HMG1_HUMAN
ID   HMG1_HUMAN     STANDARD;      PRT;   214 AA.
AC   P09429; Q6IBE1;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-AUG-1990 (Rel. 15, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   High mobility group protein 1 (HMG-1) (High mobility group protein
DE   B1).
GN   Name=HMGB1; Synonyms=HMG1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=89160247; PubMed=2922262;
RA   Wen L., Huang J.K., Johnson B.H., Reeck G.R.;
RT   "A human placental cDNA clone that encodes nonhistone chromosomal
RT   protein HMG-1.";
RL   Nucleic Acids Res. 17:1197-1214(1989).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX   MEDLINE=96299787; PubMed=8661151; DOI=10.1006/geno.1996.0369;
RA   Ferrari S., Finelli P., Rocchi M., Bianchi M.E.;
RT   "The active gene that encodes human high mobility group 1 protein
RT   (HMG1) contains introns and maps to chromosome 13.";
RL   Genomics 35:367-371(1996).
```

```
RN   [3]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RA   He F.T., Yang Z.H., Ji Q., Li R., Peng J., Jiang Y., Zhong X.;
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Small intestine;
RG   The German cDNA consortium;
RL   Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA   Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RT   "Cloning of human full open reading frames in Gateway(TM) system entry
RT   vector (pDONR201).";
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA   Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA   Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA   Phelan M., Farmer A.;
RT   "Cloning of human full-length CDSs in BD Creator(TM) system donor
RT   vector.";
RL   Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Brain, Cervix, and Testis;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [8]
RP   PROTEIN SEQUENCE OF 57-64 AND 112-126.
RC   TISSUE=Mammary carcinoma;
RX   MEDLINE=97295304; PubMed=9150946;
RA   Rasmussen R.K., Ji H., Eddes J.S., Moritz R.L., Reid G.E.,
RA   Simpson R.J., Dorow D.S.;
RT   "Two-dimensional electrophoretic analysis of human breast carcinoma
RT   proteins: mapping of proteins that bind to the SH3 domain of mixed
RT   lineage kinase MLK2.";
RL   Electrophoresis 18:588-598(1997).
CC   -!- FUNCTION: Binds preferentially single-stranded DNA and unwinds
CC       double stranded DNA.
CC   -!- INTERACTION:
CC       P04637:TP53; NbExp=1; IntAct=EBI-389432, EBI-366083;
CC       O15350:TP73; NbExp=1; IntAct=EBI-389432, EBI-389606;
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
CC   -!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; X12597; CAA31110.1; -; mRNA.
DR   EMBL; U51677; AAB08987.1; -; Genomic_DNA.
DR   EMBL; AY377859; AAQ91389.1; -; mRNA.
DR   EMBL; CR749614; CAH18408.1; -; mRNA.
DR   EMBL; CR456863; CAG33144.1; -; mRNA.
DR   EMBL; BT006940; AAP35586.1; -; mRNA.
DR   EMBL; BT020159; AAV38961.1; -; mRNA.
DR   EMBL; BC003378; AAH03378.1; -; mRNA.
DR   EMBL; BC030981; AAH30981.1; -; mRNA.
DR   EMBL; BC066889; AAH66889.1; -; mRNA.
DR   EMBL; BC067732; AAH67732.1; -; mRNA.
DR   PIR; S02826; S02826.
DR   HSSP; P07156; 1NHN.
DR   SMR; P09429; 1-83, 92-170.
DR   IntAct; P09429; -.
DR   Ensembl; ENSG00000189403; Homo sapiens.
DR   HGNC; HGNC:4983; HMGB1.
DR   H-InvDB; HIX0011209; -.
DR   MIM; 163905; -.
DR   GO; GO:0000793; C:condensed chromosome; IDA.
DR   GO; GO:0008301; F:DNA bending activity; TAS.
DR   GO; GO:0008134; F:transcription factor binding; TAS.
DR   GO; GO:0006288; P:base-excision repair, DNA ligation; IDA.
DR   GO; GO:0006310; P:DNA recombination; TAS.
DR   GO; GO:0006281; P:DNA repair; TAS.
DR   GO; GO:0006268; P:DNA unwinding; NAS.
DR   GO; GO:0006325; P:establishment and/or maintenance of chromat. . .; TAS.
DR   GO; GO:0017055; P:negative regulation of transcriptional prei. . .; IDA.
DR   GO; GO:0006357; P:regulation of transcription from RNA polyme. . .; IDA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
KW   Chromosomal protein; Direct protein sequencing; DNA-binding;
KW   Nuclear protein; Repeat.
FT   INIT_MET      0      0
FT   DNA_BIND      8     78       HMG box 1.
FT   DNA_BIND     94    162       HMG box 2.
FT   COMPBIAS    185    214       Asp/Glu-rich (acidic).
FT   CONFLICT    214    214       E -> D (in Ref. 5).
SQ   SEQUENCE   214 AA;  24763 MW;  B3C6A80FC7F0F433 CRC64;

  Query Match            99.5%;  Score 214;  DB 1;  Length 214;
  Best Local Similarity  100.0%;  Pred. No. 9.7e-184;
  Matches  214;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 60

Qy         62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 120

Qy        122 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 180

Qy        182 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||
Db        181 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 214


RESULT 5
HMG1_BOVIN
ID   HMG1_BOVIN     STANDARD;      PRT;   214 AA.
AC   P10103;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-AUG-1990 (Rel. 15, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   High mobility group protein 1 (HMG-1) (High mobility group protein
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DE   B1).
GN   Name=HMGB1; Synonyms=HMG1;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   STRAIN=Holstein; TISSUE=Fetal thymus;
RX   MEDLINE=89057489; PubMed=3194213;
RA   Kaplan D.J., Duncan C.H.;
RT   "Full length cDNA sequence for bovine high mobility group 1 (HMG1)
RT   protein.";
RL   Nucleic Acids Res. 16:10375-10375(1988).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 115-214.
RX   MEDLINE=84128872; PubMed=6141822;
RA   Pentecost B., Dixon G.H.;
RT   "Isolation and partial sequence of bovine cDNA clones for the high-
RT   mobility-group protein (HMG-1).";
RL   Biosci. Rep. 4:49-57(1984).
RN   [3]
RP   PROTEIN SEQUENCE OF 1-37; 45-156 AND 158-194.
RX   MEDLINE=81138848; PubMed=7202717; DOI=10.1016/0014-5793(80)80453-4;
RA   Walker J.M., Gooderham K., Hastings J.R., Mayes E., Johns E.W.;
RT   "The primary structures of non-histone chromosomal proteins HMG 1 and
RT   2.";
RL   FEBS Lett. 122:264-270(1980).
RN   [4]
RP   PROTEIN SEQUENCE OF 1-36.
RX   MEDLINE=90306387; PubMed=2365081; DOI=10.1016/0014-5793(90)80308-6;
RA   Christen T., Bischoff M., Hobi R., Kuenzle C.C.;
RT   "High mobility group proteins 1 and 2 bind preferentially to
RT   brominated poly(dG-dC).poly(dG-dC) in the Z-DNA conformation but not
RT   to other types of Z-DNA.";
RL   FEBS Lett. 267:139-141(1990).
CC   -!- FUNCTION: Binds preferentially single-stranded DNA and unwinds
CC       double stranded DNA.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
CC   -!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; X12796; CAA31284.1; -; mRNA.
DR   EMBL; M26110; AAA30567.1; -; mRNA.
DR   PIR; S01947; S01947.
DR   HSSP; P07156; 1NHN.
DR   SMR; P10103; 1-83, 92-170.
DR   GO; GO:0000793; C:condensed chromosome; ISS.
DR   GO; GO:0008301; F:DNA bending activity; ISS.
DR   GO; GO:0005515; F:protein binding; ISS.
DR   GO; GO:0006288; P:base-excision repair, DNA ligation; ISS.
DR   GO; GO:0006310; P:DNA recombination; ISS.
DR   GO; GO:0006281; P:DNA repair; ISS.
DR   GO; GO:0006268; P:DNA unwinding; ISS.
DR   GO; GO:0006325; P:establishment and/or maintenance of chromat. . .; ISS.
DR   GO; GO:0017055; P:negative regulation of transcriptional prei. . .; ISS.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
KW   Chromosomal protein; Direct protein sequencing; DNA-binding;
KW   Nuclear protein; Repeat.
FT   INIT_MET      0      0
FT   DNA_BIND      8     78       HMG box 1.
FT   DNA_BIND     94    162       HMG box 2.
FT   COMPBIAS    185    214       Asp/Glu-rich (acidic).
FT   CONFLICT     22     22       C -> S (in Ref. 3).
FT   CONFLICT    105    105       C -> A (in Ref. 3).
FT   CONFLICT    115    119       EHPGL -> PGGGV (in Ref. 2).
FT   CONFLICT    193    193       E -> D (in Ref. 3).
SQ   SEQUENCE   214 AA;  24777 MW;  B283A80FC7F0F433 CRC64;

  Query Match             95.3%;  Score 205;  DB 1;  Length 214;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-175;
  Matches  205;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 60

Qy         62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 120

Qy        122 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 180

Qy        182 KKKKEEEEDEEDEEDEEEEEDEEDE 206
              |||||||||||||||||||||||||
Db        181 KKKKEEEEDEEDEEDEEEEEDEEDE 205


RESULT 6
Q5T7C5_HUMAN
ID   Q5T7C5_HUMAN PRELIMINARY;      PRT;   192 AA.
AC   Q5T7C5;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   High-mobility group box 1 (Fragment).
GN   Name=HMGB1; ORFNames=RP11-550P23.1-001;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Pelan S.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL353648; CAI15602.1; -; Genomic_DNA.
DR   SMR; Q5T7C5; 2-84, 93-171.
DR   GO; GO:0000785; C:chromatin; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
FT   NON_TER     192    192
SQ   SEQUENCE   192 AA;  22050 MW;  6A52DB61DA307C1D CRC64;

  Query Match             89.3%;  Score 192;  DB 2;  Length 192;
  Best Local Similarity   100.0%;  Pred. No. 5e-164;
  Matches  192;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy         121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy         181 SKKKKEEEEDEE 192
                ||||||||||||
Db         181 SKKKKEEEEDEE 192


RESULT 7
Q9QWY6_SPAEH
ID   Q9QWY6_SPAEH PRELIMINARY;      PRT;   215 AA.
AC   Q9QWY6;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   High mobility group protein.
GN   Name=HMG1;
OS   Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Spalacinae; Nannospalax.
OX   NCBI_TaxID=30637;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Lee K.-L.D., Lum H.-K., Nevo E.;
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF078819; AAC27652.1; -; Genomic_DNA.
DR   HSSP; P07156; 1NHN.
DR   SMR; Q9QWY6; 2-84, 93-171.
DR   GO; GO:0000785; C:chromatin; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
SQ   SEQUENCE   215 AA;  24822 MW;  D20D659274B575B4 CRC64;

  Query Match             87.9%;  Score 189;  DB 2;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-161;
  Matches  189;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          27 HKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFEDMAKADKARYEREMKTYIPPKGETK 86
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          27 HKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFEDMAKADKARYEREMKTYIPPKGETK 86

Qy          87 KKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEK 146
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          87 KKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEK 146

Qy         147 KAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKSKKKKEEEEDEEDEEDEEEEEDEEDE 206
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         147 KAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKSKKKKEEEEDEEDEEDEEEEEDEEDE 206

Qy         207 DEEEDDDDE 215
                |||||||||
Db         207 DEEEDDDDE 215


RESULT 8
Q548R9_RAT
ID   Q548R9_RAT  PRELIMINARY;      PRT;   215 AA.
AC   Q548R9;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Amphoterin.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sprague-Dawley; TISSUE=Kidney;
RA   Ito T., Suzuki A., Horimoto N., Imai E., Hori M.;
RT   "Amphoterin is associated with the development of the kidney.";
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF275734; AAF82799.1; -; mRNA.
SQ   SEQUENCE   215 AA;  24894 MW;  8A868DE266D552B5 CRC64;

  Query Match             87.4%;  Score 188;  DB 2;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-160;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy          61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy         121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy         181 SKKKKEEE 188
                ||||||||
Db         181 SKKKKEEE 188


RESULT 9
Q58EV5_MOUSE
ID   Q58EV5_MOUSE PRELIMINARY;      PRT;   215 AA.
AC   Q58EV5;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   High mobility group box 1 (16 days neonate thymus cDNA, RIKEN full-
DE   length enriched library, clone:A130064K11 product:high mobility group
DE   box 1, full insert sequence) (13 days embryo heart cDNA, RIKEN full-
DE   length enriched library, clone:D330050N16 product:high mobility group
DE   box 1, full insert sequence).
GN   Name=Hmgb1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Colon, and Mammary tumor. C3;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
```

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RG NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart, and Thymus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart, and Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart, and Thymus;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart, and Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart, and Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [9]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN [10]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC091741; AAH91741.1; -; mRNA.
DR EMBL; BC094030; AAH94030.1; -; mRNA.
DR EMBL; AK037928; BAC29902.1; -; mRNA.
DR EMBL; AK084841; BAC39289.1; -; mRNA.
DR SMR; Q58EV5; 2-84, 93-171.
DR MGI; MGI:96113; Hmgb1.
DR GO; GO:0005615; C:extracellular space; IDA.
DR GO; GO:0005634; C:nucleus; TAS.
DR GO; GO:0030235; F:nitric-oxide synthase regulator activity; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0006809; P:nitric oxide biosynthesis; IDA.
DR GO; GO:0006810; P:transport; IDA.
DR InterPro; IPR000135; Highmoblty_12.

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DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
SQ   SEQUENCE   215 AA;  24894 MW;  8A868DE266D552B5 CRC64;

  Query Match             87.4%;  Score 188;  DB 2;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-160;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
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Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEE 188
              ||||||||
Db        181 SKKKKEEE 188


RESULT 10
HMG1_MOUSE
ID   HMG1_MOUSE     STANDARD;      PRT;   214 AA.
AC   P63158; P07155; P27109; P27428;
DT   01-APR-1988 (Rel. 07, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   High mobility group protein 1 (HMG-1) (High mobility group protein
DE   B1).
GN   Name=Hmgb1; Synonyms=Hmg-1, Hmg1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C3H/He;
RX   MEDLINE=92335012; PubMed=1630928;
RA   Yotov W.V., St Arnaud R.;
RT   "Nucleotide sequence of a mouse cDNA encoding the nonhistone
RT   chromosomal high mobility group protein-1 (HMG1).";
RL   Nucleic Acids Res. 20:3516-3516(1992).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=94235965; PubMed=8180479; DOI=10.1007/BF00292334;
RA   Pauken C.M., Nagle D.L., Bucan M., Lo C.W.;
RT   "Molecular cloning, expression analysis, and chromosomal localization
RT   of mouse Hmg1-containing sequences.";
RL   Mamm. Genome 5:91-99(1994).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=129/Sv; TISSUE=Liver;
RX   MEDLINE=95050689; PubMed=7961836;
RA   Ferrari S., Ronfani L., Calogero S., Bianchi M.;
RT   "The mouse gene coding for high mobility group 1 protein (HMG1).";
RL   J. Biol. Chem. 269:28803-28808(1994).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=AKR/J;
RA   Ghosh B.;
RL   Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Binds preferentially single-stranded DNA and unwinds
CC       double stranded DNA. Heparin-binding protein that has a role in
CC       the extension of neurite-type cytoplasmic processes in developing
CC       cells.
CC   -!- SUBCELLULAR LOCATION: Nuclear and also cytoplasmic, associated
CC       with the plasma membrane of filipodia in process-growing cells,
CC       and also deposited into the substrate-attached material.
CC   -!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
CC   -!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; Z11997; CAA78042.1; -; mRNA.
DR   EMBL; U00431; AAA20508.1; -; mRNA.
DR   EMBL; X80457; CAA56631.1; -; Genomic_DNA.
DR   EMBL; L38477; AAA57042.1; -; mRNA.
DR   EMBL; BC006586; AAH06586.1; -; mRNA.
DR   EMBL; BC008565; AAH08565.1; -; mRNA.
DR   EMBL; BC083067; AAH83067.1; -; mRNA.
DR   EMBL; BC085090; AAH85090.1; -; mRNA.
DR   PIR; I48688; I48688.
DR   SMR; P63158; 1-83, 92-170.
DR   MGI; MGI:96113; Hmgb1.
DR   GO; GO:0005615; C:extracellular space; IDA.
DR   GO; GO:0005634; C:nucleus; TAS.
DR   GO; GO:0030235; F:nitric-oxide synthase regulator activity; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0006809; P:nitric oxide biosynthesis; IDA.
DR   GO; GO:0006810; P:transport; IDA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
KW   Chromosomal protein; DNA-binding; Heparin-binding; Nuclear protein;
KW   Repeat.
FT   INIT_MET      0      0       By similarity.
FT   DNA_BIND      8     78       HMG box 1.
FT   DNA_BIND     94    162       HMG box 2.
FT   COMPBIAS    185    214       Asp/Glu-rich (acidic).
FT   CONFLICT    178    178       E -> V (in Ref. 4).
FT   CONFLICT    189    189       D -> E (in Ref. 3).
SQ   SEQUENCE   214 AA;  24763 MW;  B3C6A91FD6F1B133 CRC64;

  Query Match             87.0%;  Score 187;  DB 1;  Length 214;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-159;
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  Matches  187;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
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Db          1 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 60

Qy         62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
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Db         61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 120

Qy        122 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
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Db        121 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 180

Qy        182 KKKKEEE 188
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Db        181 KKKKEEE 187


RESULT 11
HMG1_RAT
ID   HMG1_RAT       STANDARD;      PRT;   214 AA.
AC   P63159; P07155; P27109; P27428;
DT   01-APR-1988 (Rel. 07, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   High mobility group protein 1 (HMG-1) (High mobility group protein B1)
DE   (Amphoterin) (Heparin-binding protein p30).
GN   Name=Hmgb1; Synonyms=Hmg-1, Hmg1;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sprague-Dawley; TISSUE=Liver;
RX   MEDLINE=88067717; PubMed=3684582;
RA   Paonessa G., Frank R., Cortese R.;
RT   "Nucleotide sequence of rat liver HMG1 cDNA.";
RL   Nucleic Acids Res. 15:9077-9077(1987).
RN   [2]
RP   SEQUENCE REVISION.
RA   Bianchi M.;
RL   Submitted (DEC-1988) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.
RX   MEDLINE=91358468; PubMed=1885601;
RA   Merenmies J., Pihlaskari R., Laitinen J., Wartiovaara J., Rauvala H.;
RT   "30-kDa heparin-binding protein of brain (amphoterin) involved in
RT   neurite outgrowth. Amino acid sequence and localization in the
RT   filopodia of the advancing plasma membrane.";
RL   J. Biol. Chem. 266:16722-16729(1991).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Kidney, Prostate, and Testis;
RG   NIH - Mammalian Gene Collection (MGC) project;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   PROTEIN SEQUENCE OF 1-20.
RX   MEDLINE=89066894; PubMed=2461949; DOI=10.1083/jcb.107.6.2293;
RA   Rauvala H., Merenmies J., Pihlaskari R., Korkolainen M., Huhtala M.L.,
RA   Panula P.;
RT   "The adhesive and neurite-promoting molecule p30: analysis of the
RT   amino-terminal sequence and production of antipeptide antibodies that
RT   detect p30 at the surface of neuroblastoma cells and of brain
RT   neurons.";
RL   J. Cell Biol. 107:2293-2305(1988).
RN   [6]
RP   STRUCTURE BY NMR OF 87-164.
RX   MEDLINE=93223672; PubMed=8467791;
RA   Weir H.M., Kraulis P.J., Hill C.S., Raine A.R.C., Laue E.D.,
RA   Thomas J.O.;
RT   "Structure of the HMG box motif in the B-domain of HMG1.";
RL   EMBO J. 12:1311-1319(1993).
RN   [7]
RP   STRUCTURE BY NMR OF 1-83.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=96118376; PubMed=8527432;
RA   Hardman C.H., Broadhurst R.W., Raine A.R.C., Grasser K.D.,
RA   Thomas J.O., Laue E.D.;
RT   "Structure of the A-domain of HMG1 and its interaction with DNA as
RT   studied by heteronuclear three- and four-dimensional NMR
RT   spectroscopy.";
RL   Biochemistry 34:16596-16607(1995).
CC   -!- FUNCTION: Binds preferentially single-stranded DNA and unwinds
CC       double stranded DNA. Heparin-binding protein that has a role in
CC       the extension of neurite-type cytoplasmic processes in developing
CC       cells.
CC   -!- SUBCELLULAR LOCATION: Nuclear and also cytoplasmic, associated
CC       with the plasma membrane of filipodia in process-growing cells,
CC       and also deposited into the substrate-attached material.
CC   -!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
CC   -!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; M64986; AAA40729.1; -; mRNA.
DR   EMBL; Y00463; CAA68526.1; -; mRNA.
DR   EMBL; BC061779; AAH61779.1; -; mRNA.
DR   EMBL; BC081839; AAH81839.1; -; mRNA.
DR   EMBL; BC088402; AAH88402.1; -; mRNA.
DR   PIR; A41175; NSRTH1.
DR   PDB; 1AAB; NMR; @=1-83.
DR   PDB; 1CKT; X-ray; A=7-77.
DR   PDB; 1HME; NMR; @=88-164.
DR   PDB; 1HMF; NMR; @=88-164.
DR   SMR; P63159; 1-83, 92-170.
DR   Ensembl; ENSRNOG00000030351; Rattus norvegicus.
DR   RGD; 2802; Hmgb1.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
KW   3D-structure; Chromosomal protein; Direct protein sequencing;
KW   DNA-binding; Heparin-binding; Nuclear protein; Repeat.
FT   INIT_MET      0      0
FT   DNA_BIND      8     78       HMG box 1.
FT   DNA_BIND     94    162       HMG box 2.
FT   COMPBIAS    185    214       Asp/Glu-rich (acidic).
FT   HELIX        14     29
FT   TURN         31     32
FT   HELIX        37     49
FT   TURN         50     50
FT   TURN         53     55
FT   HELIX        57     74
FT   TURN         75     76
FT   HELIX       100    115
FT   TURN        117    118
FT   HELIX       121    134
FT   HELIX       137    158
FT   TURN        159    160
SQ   SEQUENCE   214 AA;  24763 MW;  B3C6A91FD6F1B133 CRC64;

  Query Match             87.0%;  Score 187;  DB 1;  Length 214;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-159;
  Matches  187;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
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Db          1 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 60

Qy         62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 120

Qy        122 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
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Db        121 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 180

Qy        182 KKKKEEE 188
                 |||||||
Db        181 KKKKEEE 187


RESULT 12
Q8BNM0_MOUSE
ID   Q8BNM0_MOUSE PRELIMINARY;      PRT;   181 AA.
AC   Q8BNM0;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mus musculus 7 days embryo whole body cDNA, RIKEN full-length enriched
DE   library, clone:C430013M12 product:high mobility group box 1, full
DE   insert sequence. (Fragment).
GN   Name=Hmgb1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK082902; BAC38678.1; -; mRNA.
DR   HSSP; P07156; 1NHN.
DR   SMR; Q8BNM0; 2-84, 93-171.
DR   MGI; MGI:96113; Hmgb1.
DR   GO; GO:0005615; C:extracellular space; IDA.
DR   GO; GO:0005634; C:nucleus; TAS.
DR   GO; GO:0030235; F:nitric-oxide synthase regulator activity; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0006809; P:nitric oxide biosynthesis; IDA.
DR   GO; GO:0006810; P:transport; IDA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
FT   NON_TER     181    181
SQ   SEQUENCE   181 AA;  20648 MW;  B31D82055FD80D52 CRC64;

  Query Match           84.2%;  Score 181;  DB 2;  Length 181;
  Best Local Similarity  100.0%;  Pred. No. 3.6e-154;
  Matches  181;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 S 181
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Db        181 S 181


RESULT 13
Q8C7C4_MOUSE
ID   Q8C7C4_MOUSE PRELIMINARY;      PRT;   178 AA.
AC   Q8C7C4;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-
DE   length enriched library, clone:C920030E14 product:high mobility group
DE   box 1, full insert sequence. (Fragment).
GN   Name=Hmgb1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK050659; BAC34367.1; -; mRNA.
DR   HSSP; P07156; 1NHN.
DR   SMR; Q8C7C4; 2-84, 93-171.
DR   MGI; MGI:96113; Hmgb1.
DR   GO; GO:0005615; C:extracellular space; IDA.
DR   GO; GO:0005634; C:nucleus; TAS.
DR   GO; GO:0030235; F:nitric-oxide synthase regulator activity; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0006809; P:nitric oxide biosynthesis; IDA.
DR   GO; GO:0006810; P:transport; IDA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
FT   NON_TER     178    178
SQ   SEQUENCE   178 AA;  20303 MW;  155FD80D52960A62 CRC64;

  Query Match             82.8%;  Score 178;  DB 2;  Length 178;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-151;
  Matches  178;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKA 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKA 178


RESULT 14
Q9QX40_SPAEH
ID   Q9QX40_SPAEH PRELIMINARY;      PRT;   215 AA.
AC   Q9QX40;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   High mobility group protein.
GN   Name=HMG1;
OS   Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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OC   Muridae; Spalacinae; Nannospalax.
OX   NCBI_TaxID=30637;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Lee K.-L.D., Lum H.-K., Nevo E.;
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF078820; AAC27653.2; -; Genomic_DNA.
DR   HSSP; P07156; 1NHN.
DR   SMR; Q9QX40; 2-84, 93-171.
DR   GO; GO:0000785; C:chromatin; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
SQ   SEQUENCE   215 AA;  24895 MW;  599FB8A6FDF41F17 CRC64;

  Query Match             74.4%;  Score 160;  DB 2;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 3e-135;
  Matches  160;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         56 EKGKFEDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKG 115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         56 EKGKFEDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKG 115

Qy        116 EHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGV 175
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        116 EHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGV 175

Qy        176 VKAEKSKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||||||||
Db        176 VKAEKSKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 15
Q5T7C2_HUMAN
ID   Q5T7C2_HUMAN PRELIMINARY;      PRT;   157 AA.
AC   Q5T7C2;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   High-mobility group box 1 (Fragment).
GN   Name=HMGB1; ORFNames=RP11-550P23.1-009;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Pelan S.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL353648; CAI15604.1; -; Genomic_DNA.
DR   SMR; Q5T7C2; 2-84, 89-157.
DR   GO; GO:0000785; C:chromatin; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
FT   NON_TER     157    157
SQ   SEQUENCE   157 AA;  18164 MW;  F38343E7F52FC457 CRC64;

  Query Match             73.0%;  Score 157;  DB 2;  Length 157;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-132;
  Matches  157;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEK 157
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Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEK 157


Search completed: April  6, 2006, 10:40:42
Job time : 231 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 10:40:58 ; Search time 46 Seconds
(without alignments)
386.419 Million cell updates/sec

Title: US-10-717-984-1
Perfect score: 215
Sequence: 1 MGKGDPKKPRGKMSSYAFFV.....DEEEEEDEEDEDEEEDDDDE 215

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 1

Total number of hits satisfying chosen parameters: 570988

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	214	99.5	214	2	US-09-538-092-883	Sequence 883, App
2	214	99.5	214	2	US-09-214-881A-1	Sequence 1, Appli
3	205	95.3	214	2	US-09-214-881A-3	Sequence 3, Appli
4	140	65.1	214	2	US-09-214-881A-4	Sequence 4, Appli
5	140	65.1	214	2	US-09-214-881A-5	Sequence 5, Appli
6	98	45.6	101	2	US-09-513-999C-7904	Sequence 7904, Ap
7	92	42.8	213	2	US-09-949-016-10813	Sequence 10813, A
8	90	41.9	110	2	US-09-513-999C-4824	Sequence 4824, Ap
9	61	28.4	110	2	US-09-513-999C-4825	Sequence 4825, Ap
10	39	18.1	59	2	US-09-513-999C-4826	Sequence 4826, Ap
11	30	14.0	30	1	US-08-803-545-1	Sequence 1, Appli
12	26	12.1	208	2	US-09-538-092-1018	Sequence 1018, Ap
13	26	12.1	208	2	US-09-214-881A-2	Sequence 2, Appli
14	26	12.1	209	2	US-09-214-881A-6	Sequence 6, Appli
15	26	12.1	209	2	US-09-214-881A-8	Sequence 8, Appli
16	26	12.1	320	2	US-09-949-016-10728	Sequence 10728, A
17	22	10.2	208	2	US-09-214-881A-11	Sequence 11, Appl
18	22	10.2	879	2	US-09-914-259-38	Sequence 38, Appl
19	21	9.8	32	2	US-09-214-881A-13	Sequence 13, Appl
20	19	8.8	206	2	US-09-214-881A-9	Sequence 9, Appli
21	18	8.4	18	1	US-08-630-645-11	Sequence 11, Appl
22	18	8.4	18	2	US-08-766-596A-11	Sequence 11, Appl
23	18	8.4	18	4	PCT-US96-10220-11	Sequence 11, Appl
24	16	7.4	185	2	US-09-214-881A-7	Sequence 7, Appli
25	15	7.0	16	1	US-08-036-555B-8	Sequence 8, Appli
26	15	7.0	16	1	US-08-469-569-8	Sequence 8, Appli
27	15	7.0	16	1	US-08-249-322A-8	Sequence 8, Appli
28	15	7.0	16	1	US-08-469-526A-8	Sequence 8, Appli
29	15	7.0	16	1	US-08-734-591A-8	Sequence 8, Appli
30	15	7.0	16	1	US-08-469-660-8	Sequence 8, Appli
31	15	7.0	16	2	US-08-470-335-8	Sequence 8, Appli
32	15	7.0	16	2	US-08-735-021-8	Sequence 8, Appli
33	15	7.0	16	2	US-08-734-664A-8	Sequence 8, Appli
34	15	7.0	16	2	US-08-470-339-8	Sequence 8, Appli
35	15	7.0	16	2	US-08-467-602-8	Sequence 8, Appli
36	15	7.0	16	4	PCT-US94-05083C-8	Sequence 8, Appli
37	15	7.0	16	4	PCT-US95-06846A-8	Sequence 8, Appli
38	15	7.0	32	2	US-09-214-881A-12	Sequence 12, Appl
39	15	7.0	122	2	US-09-513-999C-4966	Sequence 4966, Ap
40	15	7.0	200	2	US-09-702-705-324	Sequence 324, App
41	15	7.0	200	2	US-09-702-705-789	Sequence 789, App
42	15	7.0	200	2	US-09-736-457-324	Sequence 324, App
43	15	7.0	200	2	US-09-736-457-789	Sequence 789, App
44	15	7.0	200	2	US-09-614-124B-324	Sequence 324, App
45	15	7.0	200	2	US-09-614-124B-789	Sequence 789, App

ALIGNMENTS

RESULT 1
US-09-538-092-883
; Sequence 883, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 883
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P09429
US-09-538-092-883

Query Match 99.5%; Score 214; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 2.6e-187;
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 60

Qy         62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 120

Qy        122 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 180

Qy        182 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||
Db        181 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 214
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RESULT 2
US-09-214-881A-1

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; Sequence 1, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
;  APPLICANT:  Ozaki, Shoichi
;  APPLICANT:  Sobajima, Junko
;  APPLICANT:  Uesugi, Hiroko
;  APPLICANT:  Okazaki, Takahiro
;  APPLICANT:  Tanaka, Masao
;  APPLICANT:  Nakao, Kazuwa
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION:  DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE:  068383.0104
;  CURRENT APPLICATION NUMBER: US/09/214,881A
;  CURRENT FILING DATE:  1999-06-07
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 214
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-214-881A-1

  Query Match            99.5%;  Score 214;  DB 2;  Length 214;
  Best Local Similarity  100.0%;  Pred. No. 2.6e-187;
  Matches  214;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 60

Qy         62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 120

Qy        122 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 180

Qy        182 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||
Db        181 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 214


RESULT 3
US-09-214-881A-3
; Sequence 3, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
;  APPLICANT:  Ozaki, Shoichi
;  APPLICANT:  Sobajima, Junko
;  APPLICANT:  Uesugi, Hiroko
;  APPLICANT:  Okazaki, Takahiro
;  APPLICANT:  Tanaka, Masao
;  APPLICANT:  Nakao, Kazuwa
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION:  DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE:  068383.0104
;  CURRENT APPLICATION NUMBER: US/09/214,881A
;  CURRENT FILING DATE:  1999-06-07
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 214
;   TYPE: PRT
;   ORGANISM: Bos taurus
US-09-214-881A-3

  Query Match            95.3%;  Score 205;  DB 2;  Length 214;
  Best Local Similarity  100.0%;  Pred. No. 4.2e-179;
  Matches  205;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 60

Qy         62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 120

Qy        122 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 180

Qy        182 KKKKEEEEDEEDEEDEEEEEDEEDE 206
              |||||||||||||||||||||||||
Db        181 KKKKEEEEDEEDEEDEEEEEDEEDE 205


RESULT 4
US-09-214-881A-4
; Sequence 4, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
;  APPLICANT:  Ozaki, Shoichi
;  APPLICANT:  Sobajima, Junko
;  APPLICANT:  Uesugi, Hiroko
;  APPLICANT:  Okazaki, Takahiro
;  APPLICANT:  Tanaka, Masao
;  APPLICANT:  Nakao, Kazuwa
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION:  DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE:  068383.0104
;  CURRENT APPLICATION NUMBER: US/09/214,881A
;  CURRENT FILING DATE:  1999-06-07
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 214
;   TYPE: PRT
;   ORGANISM: Sus scrofa
US-09-214-881A-4

  Query Match            65.1%;  Score 140;  DB 2;  Length 214;
  Best Local Similarity  100.0%;  Pred. No. 7.1e-120;
  Matches  140;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 60

Qy         62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 120

Qy        122 IGDVAKKLGEMWNNTAADDK 141
              ||||||||||||||||||||
Db        121 IGDVAKKLGEMWNNTAADDK 140


RESULT 5
US-09-214-881A-5
; Sequence 5, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
;  APPLICANT:  Ozaki, Shoichi
;  APPLICANT:  Sobajima, Junko
;  APPLICANT:  Uesugi, Hiroko
;  APPLICANT:  Okazaki, Takahiro
;  APPLICANT:  Tanaka, Masao
;  APPLICANT:  Nakao, Kazuwa
```

```
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION:  DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE:  068383.0104
;  CURRENT APPLICATION NUMBER: US/09/214,881A
;  CURRENT FILING DATE:  1999-06-07
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 214
;   TYPE: PRT
;   ORGANISM: Rattus rattus
US-09-214-881A-5

  Query Match             65.1%;  Score 140;  DB 2;  Length 214;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-120;
  Matches  140;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 60

Qy         62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 120

Qy        122 IGDVAKKLGEMWNNTAADDK 141
              ||||||||||||||||||||
Db        121 IGDVAKKLGEMWNNTAADDK 140


RESULT 6
US-09-513-999C-7904
; Sequence 7904, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 7904
;   LENGTH: 101
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-513-999C-7904

  Query Match             45.6%;  Score 98;  DB 2;  Length 101;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-82;
  Matches   98;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRP 98
              |||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRP 98


RESULT 7
US-09-949-016-10813
; Sequence 10813, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10813
;   LENGTH: 213
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-10813

  Query Match             42.8%;  Score 92;  DB 2;  Length 213;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-76;
  Matches   92;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        109 YRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKP 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 YRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKP 170

Qy        169 DAAKKGVVKAEKSKKKKEEEEDEEDEEDEEEE 200
              ||||||||||||||||||||||||||||||||
Db        171 DAAKKGVVKAEKSKKKKEEEEDEEDEEDEEEE 202


RESULT 8
US-09-513-999C-4824
; Sequence 4824, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 4824
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: UNSURE
;   LOCATION: 91
;   OTHER INFORMATION: Xaa=Asp or Gly
US-09-513-999C-4824

  Query Match             41.9%;  Score 90;  DB 2;  Length 110;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-74;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFK 90
              ||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFK 90
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RESULT 9
US-09-513-999C-4825
; Sequence 4825, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 4825
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: UNSURE
;   LOCATION: 12
;   OTHER INFORMATION: Xaa=Glu or Lys
;   FEATURE:
;   NAME/KEY: UNSURE
;   LOCATION: 17
;   OTHER INFORMATION: Xaa=Ala or Gly
;   FEATURE:
;   NAME/KEY: UNSURE
;   LOCATION: 29
;   OTHER INFORMATION: Xaa=Lys or Arg
;   FEATURE:
;   NAME/KEY: UNSURE
;   LOCATION: 91
;   OTHER INFORMATION: Xaa=Asp or Gly
US-09-513-999C-4825

  Query Match             28.4%;  Score 61;  DB 2;  Length 110;
  Best Local Similarity   100.0%;  Pred. No. 4e-48;
  Matches   61;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         30 KHPDASVNFSEFSKKCSERWKTMSAKEKGKFEDMAKADKARYEREMKTYIPPKGETKKKF 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         30 KHPDASVNFSEFSKKCSERWKTMSAKEKGKFEDMAKADKARYEREMKTYIPPKGETKKKF 89

Qy         90 K 90
              |
Db         90 K 90


RESULT 10
US-09-513-999C-4826
; Sequence 4826, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Duclert, A.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
;  FILE REFERENCE: 59.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/513,999C
;  CURRENT FILING DATE:  2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/122,487
;  PRIOR FILING DATE: 1999-02-26
;  NUMBER OF SEQ ID NOS: 36681
;  SOFTWARE: Patent.pm
; SEQ ID NO 4826
;   LENGTH: 59
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-513-999C-4826

  Query Match             18.1%;  Score 39;  DB 2;  Length 59;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-28;
  Matches   39;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         52 MSAKEKGKFEDMAKADKARYEREMKTYIPPKGETKKKFK 90
              |||||||||||||||||||||||||||||||||||||||||
Db          1 MSAKEKGKFEDMAKADKARYEREMKTYIPPKGETKKKFK 39


RESULT 11
US-08-803-545-1
; Sequence 1, Application US/08803545
; Patent No. 5851986
;  GENERAL INFORMATION:
;    APPLICANT:  TAKADA, Yukihiro
;    APPLICANT:  YAMAMURA, Junichi
;    APPLICANT:  GOTO, Masaaki
;    APPLICANT:  AOE, Seiichiro
;    TITLE OF INVENTION:  An Agent Promoting Bone Formation and
;    TITLE OF INVENTION:  Inhibiting Bone Resorption
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Testa, Hurwitz & Thibeault
;      STREET:  125 High St.
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/803,545
;      FILING DATE:  20-FEB-1997
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CAMPBELL, Paula A.
;      REGISTRATION NUMBER:  32,503
;      REFERENCE/DOCKET NUMBER:  FJN-054
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-7000
;      TELEFAX:  (617) 248-7100
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-803-545-1

  Query Match             14.0%;  Score 30;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-20;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKH 31
              ||||||||||||||||||||||||||||||
Db          1 GKGDPKKPRGKMSSYAFFVQTCREEHKKKH 30


RESULT 12
US-09-538-092-1018
; Sequence 1018, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
;  APPLICANT: Giot, Loic
;  APPLICANT:  Mansfield, Traci A.
;  TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
;  FILE REFERENCE: 15966-542
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;  CURRENT APPLICATION NUMBER: US/09/538,092
;  CURRENT FILING DATE:  2000-03-29
;  PRIOR APPLICATION NUMBER: 60/127,352
;  PRIOR FILING DATE: 1999-04-01
;  PRIOR APPLICATION NUMBER: 60/178,965
;  PRIOR FILING DATE: 2000-02-01
;  NUMBER OF SEQ ID NOS: 1387
;  SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1018
;   LENGTH: 208
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Polypeptide Accession Number P26583
US-09-538-092-1018

  Query Match             12.1%;  Score 26;  DB 2;  Length 208;
  Best Local Similarity   100.0%;  Pred. No. 5.3e-16;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 KPRGKMSSYAFFVQTCREEHKKKHPD 33
              |||||||||||||||||||||||||
Db          7 KPRGKMSSYAFFVQTCREEHKKKHPD 32


RESULT 13
US-09-214-881A-2
; Sequence 2, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
;  APPLICANT:  Ozaki, Shoichi
;  APPLICANT:  Sobajima, Junko
;  APPLICANT:  Uesugi, Hiroko
;  APPLICANT:  Okazaki, Takahiro
;  APPLICANT:  Tanaka, Masao
;  APPLICANT:  Nakao, Kazuwa
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION:  DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE:  068383.0104
;  CURRENT APPLICATION NUMBER: US/09/214,881A
;  CURRENT FILING DATE:  1999-06-07
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 208
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-214-881A-2

  Query Match             12.1%;  Score 26;  DB 2;  Length 208;
  Best Local Similarity   100.0%;  Pred. No. 5.3e-16;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 KPRGKMSSYAFFVQTCREEHKKKHPD 33
              |||||||||||||||||||||||||
Db          7 KPRGKMSSYAFFVQTCREEHKKKHPD 32


RESULT 14
US-09-214-881A-6
; Sequence 6, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
;  APPLICANT:  Ozaki, Shoichi
;  APPLICANT:  Sobajima, Junko
;  APPLICANT:  Uesugi, Hiroko
;  APPLICANT:  Okazaki, Takahiro
;  APPLICANT:  Tanaka, Masao
;  APPLICANT:  Nakao, Kazuwa
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION:  DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE:  068383.0104
;  CURRENT APPLICATION NUMBER: US/09/214,881A
;  CURRENT FILING DATE:  1999-06-07
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 209
;   TYPE: PRT
;   ORGANISM: Sus scrofa
US-09-214-881A-6

  Query Match             12.1%;  Score 26;  DB 2;  Length 209;
  Best Local Similarity   100.0%;  Pred. No. 5.3e-16;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 KPRGKMSSYAFFVQTCREEHKKKHPD 33
              |||||||||||||||||||||||||
Db          7 KPRGKMSSYAFFVQTCREEHKKKHPD 32


RESULT 15
US-09-214-881A-8
; Sequence 8, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
;  APPLICANT:  Ozaki, Shoichi
;  APPLICANT:  Sobajima, Junko
;  APPLICANT:  Uesugi, Hiroko
;  APPLICANT:  Okazaki, Takahiro
;  APPLICANT:  Tanaka, Masao
;  APPLICANT:  Nakao, Kazuwa
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION:  DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE:  068383.0104
;  CURRENT APPLICATION NUMBER: US/09/214,881A
;  CURRENT FILING DATE:  1999-06-07
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 209
;   TYPE: PRT
;   ORGANISM: Rattus rattus
US-09-214-881A-8

  Query Match             12.1%;  Score 26;  DB 2;  Length 209;
  Best Local Similarity   100.0%;  Pred. No. 5.3e-16;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 KPRGKMSSYAFFVQTCREEHKKKHPD 33
              |||||||||||||||||||||||||
Db          7 KPRGKMSSYAFFVQTCREEHKKKHPD 32


Search completed: April  6, 2006, 10:42:22
Job time : 47 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 10:41:43 ; Search time 167 Seconds
(without alignments)
537.924 Million cell updates/sec

Title: US-10-717-984-1
Perfect score: 215
Sequence: 1 MGKGDPKKPRGKMSSYAFFV.....DEEEEEDEEDEDEEEDDDDE 215

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size : 1

Total number of hits satisfying chosen parameters: 1866650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	215	100.0	215	4	US-10-087-192-1446	Sequence 1446, Ap
2	215	100.0	215	4	US-10-147-447-1	Sequence 1, Appli
3	215	100.0	215	4	US-10-300-072-1	Sequence 1, Appli
4	215	100.0	215	4	US-10-456-949-1	Sequence 1, Appli
5	215	100.0	215	4	US-10-456-947-1	Sequence 1, Appli
6	215	100.0	215	4	US-10-718-495-1	Sequence 1, Appli
7	215	100.0	215	4	US-10-717-984-1	Sequence 1, Appli
8	215	100.0	215	5	US-10-868-577A-63	Sequence 63, Appl
9	215	100.0	215	5	US-10-868-549-22	Sequence 22, Appl
10	215	100.0	215	5	US-10-938-992-74	Sequence 74, Appl
11	214	99.5	214	3	US-09-214-881A-1	Sequence 1, Appli
12	214	99.5	214	5	US-10-726-195-1	Sequence 1, Appli
13	214	99.5	221	5	US-10-938-992-40	Sequence 40, Appl
14	206	95.8	215	5	US-10-938-992-38	Sequence 38, Appl
15	205	95.3	214	3	US-09-214-881A-3	Sequence 3, Appli
16	205	95.3	214	5	US-10-726-195-3	Sequence 3, Appli
17	188	87.4	215	4	US-10-147-447-2	Sequence 2, Appli
18	188	87.4	215	4	US-10-300-072-2	Sequence 2, Appli
19	188	87.4	215	4	US-10-456-949-2	Sequence 2, Appli
20	188	87.4	215	4	US-10-456-947-2	Sequence 2, Appli
21	188	87.4	215	4	US-10-718-495-2	Sequence 2, Appli
22	188	87.4	215	4	US-10-717-984-2	Sequence 2, Appli
23	188	87.4	215	5	US-10-938-992-18	Sequence 18, Appl
24	188	87.4	220	4	US-10-087-192-1443	Sequence 1443, Ap
25	188	87.4	252	5	US-10-938-992-5	Sequence 5, Appli
26	156	72.6	178	4	US-10-264-049-3323	Sequence 3323, Ap
27	153	71.2	180	5	US-10-938-992-36	Sequence 36, Appl
28	147	68.4	176	4	US-10-094-749-2948	Sequence 2948, Ap
29	141	65.6	215	5	US-10-938-992-37	Sequence 37, Appl
30	140	65.1	214	3	US-09-214-881A-4	Sequence 4, Appli
31	140	65.1	214	3	US-09-214-881A-5	Sequence 5, Appli
32	140	65.1	214	5	US-10-726-195-4	Sequence 4, Appli
33	140	65.1	214	5	US-10-726-195-5	Sequence 5, Appli
34	137	63.7	215	6	US-11-013-684-17	Sequence 17, Appl
35	118	54.9	128	3	US-09-925-300-1757	Sequence 1757, Ap
36	117	54.4	121	3	US-09-925-299-1055	Sequence 1055, Ap
37	117	54.4	121	3	US-09-925-299-1055	Sequence 1055, Ap
38	116	54.0	128	4	US-10-106-698-6757	Sequence 6757, Ap
39	108	50.2	216	4	US-10-147-447-18	Sequence 18, Appl
40	108	50.2	216	4	US-10-300-072-18	Sequence 18, Appl
41	108	50.2	216	4	US-10-300-072-24	Sequence 24, Appl
42	108	50.2	216	4	US-10-456-949-18	Sequence 18, Appl
43	108	50.2	216	4	US-10-456-947-6	Sequence 6, Appli
44	108	50.2	216	4	US-10-456-947-10	Sequence 10, Appl
45	108	50.2	216	4	US-10-718-495-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-10-087-192-1446
; Sequence 1446, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1446
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-192-1446

Query Match 100.0%; Score 215; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 6e-173;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
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Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
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Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
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RESULT 2
US-10-147-447-1
; Sequence 1, Application US/10147447
; Publication No. US20030060410A1
; GENERAL INFORMATION:

```
;  APPLICANT: Tracey, Kevin J.
;  APPLICANT:  Yang, Huan
;  APPLICANT:  Warren Jr., Howland Shaw
;  APPLICANT:  Fink, Mitchell P.
;  TITLE OF INVENTION: Use of HMG Fragments as
;  TITLE OF INVENTION:  Anti-Inflammatory Agents
;  FILE REFERENCE: 3268.1001-001
;  CURRENT APPLICATION NUMBER: US/10/147,447
;  CURRENT FILING DATE:  2002-08-16
;  PRIOR APPLICATION NUMBER: 60/291,034
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-147-447-1

  Query Match             100.0%;  Score 215;  DB 4;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 6e-173;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 3
US-10-300-072-1
; Sequence 1, Application US/10300072
; Publication No. US20030144201A1
; GENERAL INFORMATION:
;  APPLICANT: Kevin J. Tracey
;  APPLICANT:  Huan Yang
;  APPLICANT:  Howland Shaw Warren, Jr.
;  APPLICANT:  Mitchell P. Fink
;  TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS ANTI-FLAMMATORY
;  TITLE OF INVENTION:  AGENTS
;  FILE REFERENCE: 3268.1001-005
;  CURRENT APPLICATION NUMBER: US/10/300,072
;  CURRENT FILING DATE:  2002-11-20
;  PRIOR APPLICATION NUMBER: US 10/147,447
;  PRIOR FILING DATE: 2002-05-15
;  PRIOR APPLICATION NUMBER: US 60/291,034
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-300-072-1

  Query Match             100.0%;  Score 215;  DB 4;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 6e-173;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
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Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
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Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
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RESULT 4
US-10-456-949-1
; Sequence 1, Application US/10456949
; Publication No. US20040005316A1
; GENERAL INFORMATION:
;  APPLICANT: Kevin J. Tracey
;  APPLICANT:  Huan Yang
;  TITLE OF INVENTION: USE OF HMG FRAGMENTS AS
;  TITLE OF INVENTION:  ANTI-INFLAMMATORY AGENTS
;  FILE REFERENCE: 3268.1001-006
;  CURRENT APPLICATION NUMBER: US/10/456,949
;  CURRENT FILING DATE:  2003-06-06
;  PRIOR APPLICATION NUMBER: 10/147,447
;  PRIOR FILING DATE: 2002-05-15
;  PRIOR APPLICATION NUMBER: 60/291,034
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-456-949-1

  Query Match             100.0%;  Score 215;  DB 4;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 6e-173;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
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Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
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Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
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Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 5
US-10-456-947-1
; Sequence 1, Application US/10456947
; Publication No. US20040053841A1
; GENERAL INFORMATION:
;  APPLICANT: Kevin J. Tracey
;  APPLICANT:  Huan Yang
;  TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN
;  TITLE OF INVENTION:  HMGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS
;  TITLE OF INVENTION:  ANTI-INFLAMMATORY AGENTS
;  FILE REFERENCE: 3268.1001-007
;  CURRENT APPLICATION NUMBER: US/10/456,947
;  CURRENT FILING DATE:  2003-06-06
;  PRIOR APPLICATION NUMBER: 10/147,447
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;  PRIOR FILING DATE: 2002-05-15
;  PRIOR APPLICATION NUMBER: 60/291,034
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-456-947-1

  Query Match            100.0%;  Score 215;  DB 4;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 6e-173;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
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Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
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Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
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Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 6
US-10-718-495-1
; Sequence 1, Application US/10718495
; Publication No. US20040141948A1
; GENERAL INFORMATION:
;  APPLICANT: O'Keefe, Theresa L.
;  TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS
;  TITLE OF INVENTION:  ANTI-INFLAMMATORY AGENTS
;  FILE REFERENCE: 3258.1009-001
;  CURRENT APPLICATION NUMBER: US/10/718,495
;  CURRENT FILING DATE:  2003-11-12
;  PRIOR APPLICATION NUMBER: 60/427,841
;  PRIOR FILING DATE: 2002-11-20
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-718-495-1

  Query Match            100.0%;  Score 215;  DB 4;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 6e-173;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 7
US-10-717-984-1
; Sequence 1, Application US/10717984
; Publication No. US20040156851A1
; GENERAL INFORMATION:
;  APPLICANT: Newman, Walter
;  TITLE OF INVENTION: HMGB1 COMBINATION THERAPIES
;  FILE REFERENCE: 3258.1008-001
;  CURRENT APPLICATION NUMBER: US/10/717,984
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,846
;  PRIOR FILING DATE: 2002-11-20
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-717-984-1

  Query Match            100.0%;  Score 215;  DB 4;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 6e-173;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 8
US-10-868-577A-63
; Sequence 63, Application US/10868577A
; Publication No. US20050032697A1
; GENERAL INFORMATION:
;  APPLICANT: Alitalo et al.
;  TITLE OF INVENTION: HEPARIN BINDING VEGFR-3 LIGANDS
;  FILE REFERENCE: 28967/39359A
;  CURRENT APPLICATION NUMBER: US/10/868,577A
;  CURRENT FILING DATE:  2004-06-14
;  PRIOR APPLICATION NUMBER: US 60/478,390
;  PRIOR FILING DATE: 2003-06-12
;  PRIOR APPLICATION NUMBER: US 10/669,176
;  PRIOR FILING DATE: 2003-09-23
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-868-577A-63

  Query Match            100.0%;  Score 215;  DB 5;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 6e-173;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy         121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy         181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
                |||||||||||||||||||||||||||||||||||
Db         181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 9
US-10-868-549-22
; Sequence 22, Application US/10868549
; Publication No. US20050043235A1
; GENERAL INFORMATION:
;  APPLICANT: Alitalo et al.
;  TITLE OF INVENTION: USE OF VEGF-C OR VEGF-D IN RECONSTRUCTIVE SURGERY
;  FILE REFERENCE: 28967/39117A
;  CURRENT APPLICATION NUMBER: US/10/868,549
;  CURRENT FILING DATE:  2004-06-14
;  PRIOR APPLICATION NUMBER: US 60/478,114
;  PRIOR FILING DATE: 2003-06-12
;  PRIOR APPLICATION NUMBER: US 60/478,390
;  PRIOR FILING DATE: 2003-06-12
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-868-549-22

  Query Match             100.0%;  Score 215;  DB 5;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 6e-173;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy          61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy         121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy         181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
                |||||||||||||||||||||||||||||||||||
Db         181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 10
US-10-938-992-74
; Sequence 74, Application US/10938992
; Publication No. US20050152903A1
; GENERAL INFORMATION:
;  APPLICANT: Newman, Walter
;  APPLICANT:  Qin, Shixin
;  APPLICANT:  O'Keefe, Theresa
;  APPLICANT:  Obar, Robert
;  TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1
;  FILE REFERENCE: 3258.1033-001
;  CURRENT APPLICATION NUMBER: US/10/938,992
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: 60/502,568
;  PRIOR FILING DATE: 2003-09-11
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 74
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-938-992-74

  Query Match             100.0%;  Score 215;  DB 5;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 6e-173;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy          61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy         121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy         181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
                |||||||||||||||||||||||||||||||||||
Db         181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 11
US-09-214-881A-1
; Sequence 1, Application US/09214881A
; Patent No. US20020009749A1
; GENERAL INFORMATION:
;  APPLICANT:  Ozaki, Shoichi
;  APPLICANT:  Sobajima, Junko
;  APPLICANT:  Uesugi, Hiroko
;  APPLICANT:  Okazaki, Takahiro
;  APPLICANT:  Tanaka, Masao
;  APPLICANT:  Nakao, Kazuwa
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION:  DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE:  068383.0104
;  CURRENT APPLICATION NUMBER: US/09/214,881A
;  CURRENT FILING DATE:  1999-06-07
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 214
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-214-881A-1

  Query Match             99.5%;  Score 214;  DB 3;  Length 214;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-172;
  Matches  214;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 60

Qy          62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 120

Qy         122 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 180

Qy         182 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
                |||||||||||||||||||||||||||||||||||
Db         181 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 214
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RESULT 12
US-10-726-195-1
; Sequence 1, Application US/10726195
; Publication No. US20040229279A1
; GENERAL INFORMATION:
;  APPLICANT: Ozaki, Shoichi
;  APPLICANT:  Sobajima, Junko
;  APPLICANT:  Uesugi, Hiroko
;  APPLICANT:  Okazaki, Takahiro
;  APPLICANT:  Tanaka, Masao
;  APPLICANT:  Nakao, Kazuwa
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE: 068383.0104
;  CURRENT APPLICATION NUMBER: US/10/726,195
;  CURRENT FILING DATE:  2003-12-02
;  PRIOR APPLICATION NUMBER: US/09/214,881A
;  PRIOR FILING DATE: 1999-06-07
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 214
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-726-195-1

  Query Match             99.5%;  Score 214;  DB 5;  Length 214;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-172;
  Matches  214;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 60

Qy         62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 120

Qy        122 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 180

Qy        182 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||
Db        181 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 214


RESULT 13
US-10-938-992-40
; Sequence 40, Application US/10938992
; Publication No. US20050152903A1
; GENERAL INFORMATION:
;  APPLICANT: Newman, Walter
;  APPLICANT:  Qin, Shixin
;  APPLICANT:  O'Keefe, Theresa
;  APPLICANT:  Obar, Robert
;  TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1
;  FILE REFERENCE: 3258.1033-001
;  CURRENT APPLICATION NUMBER: US/10/938,992
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: 60/502,568
;  PRIOR FILING DATE: 2003-09-11
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40
;   LENGTH: 221
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: rec-HMGB1-His6
US-10-938-992-40

  Query Match             99.5%;  Score 214;  DB 5;  Length 221;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-172;
  Matches  214;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 67

Qy         62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 127

Qy        122 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 187

Qy        182 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||
Db        188 KKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 221


RESULT 14
US-10-938-992-38
; Sequence 38, Application US/10938992
; Publication No. US20050152903A1
; GENERAL INFORMATION:
;  APPLICANT: Newman, Walter
;  APPLICANT:  Qin, Shixin
;  APPLICANT:  O'Keefe, Theresa
;  APPLICANT:  Obar, Robert
;  TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1
;  FILE REFERENCE: 3258.1033-001
;  CURRENT APPLICATION NUMBER: US/10/938,992
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: 60/502,568
;  PRIOR FILING DATE: 2003-09-11
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Bos taurus
US-10-938-992-38

  Query Match             95.8%;  Score 206;  DB 5;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-165;
  Matches  206;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDE 206
              ||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDE 206


RESULT 15
US-09-214-881A-3
; Sequence 3, Application US/09214881A
; Patent No. US20020009749A1
; GENERAL INFORMATION:
;  APPLICANT:  Ozaki, Shoichi
;  APPLICANT:  Sobajima, Junko
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;  APPLICANT:  Uesugi, Hiroko
;  APPLICANT:  Okazaki, Takahiro
;  APPLICANT:  Tanaka, Masao
;  APPLICANT:  Nakao, Kazuwa
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION:  DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE:  068383.0104
;  CURRENT APPLICATION NUMBER: US/09/214,881A
;  CURRENT FILING DATE:  1999-06-07
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 214
;   TYPE: PRT
;   ORGANISM: Bos taurus
US-09-214-881A-3

  Query Match             95.3%;  Score 205;  DB 3;  Length 214;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-164;
  Matches  205;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFE 60

Qy         62 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLS 120

Qy        122 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 IGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEKS 180

Qy        182 KKKKEEEEDEEDEEDEEEEEDEEDE 206
              |||||||||||||||||||||||||
Db        181 KKKKEEEEDEEDEEDEEEEEDEEDE 205


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Job time : 168 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 10:42:38 ; Search time 24 Seconds
(without alignments)
279.428 Million cell updates/sec

Title: US-10-717-984-1
Perfect score: 215
Sequence: 1 MGKGDPKKPRGKMSSYAFFV.....DEEEEEDEEDEDEEEDDDDE 215

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

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2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /SIDS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	215	100.0	215	6	US-10-821-234-1443	Sequence 1443, Ap
2	215	100.0	215	7	US-11-186-422-11	Sequence 11, Appl
3	188	87.4	215	7	US-11-186-422-12	Sequence 12, Appl
4	69	32.1	69	7	US-11-186-422-14	Sequence 14, Appl
5	54	25.1	54	6	US-10-719-150-6	Sequence 6, Appli
6	54	25.1	54	7	US-11-186-422-13	Sequence 13, Appl
7	22	10.2	879	7	US-11-169-041-192	Sequence 192, App
8	20	9.3	169	6	US-10-821-234-1234	Sequence 1234, Ap
9	14	6.5	14	6	US-10-719-150-1	Sequence 1, Appli
10	14	6.5	15	6	US-10-719-150-4	Sequence 4, Appli
11	13	6.0	1163	7	US-11-044-899-2	Sequence 2, Appli
12	13	6.0	1163	7	US-11-044-899-30	Sequence 30, Appl
13	13	6.0	1750	7	US-11-087-099-12397	Sequence 12397, A
14	12	5.6	447	7	US-11-096-568A-28367	Sequence 28367, A
15	10	4.7	106	7	US-11-096-568A-6675	Sequence 6675, Ap
16	10	4.7	417	7	US-11-087-099-12021	Sequence 12021, A
17	10	4.7	593	7	US-11-040-488-2	Sequence 2, Appli
18	10	4.7	1531	6	US-10-330-773-142	Sequence 142, App
19	9	4.2	9	7	US-11-257-286-18	Sequence 18, Appl
20	9	4.2	106	7	US-11-087-099-7075	Sequence 7075, Ap
21	9	4.2	124	7	US-11-096-568A-9681	Sequence 9681, Ap
22	9	4.2	135	7	US-11-087-099-11504	Sequence 11504, A
23	9	4.2	137	7	US-11-096-568A-3511	Sequence 3511, Ap
24	9	4.2	139	7	US-11-096-568A-13611	Sequence 13611, A
25	9	4.2	139	7	US-11-096-568A-26884	Sequence 26884, A
26	9	4.2	140	7	US-11-172-740-1564	Sequence 1564, Ap
27	9	4.2	141	7	US-11-087-099-3073	Sequence 3073, Ap
28	9	4.2	141	7	US-11-087-099-9185	Sequence 9185, Ap
29	9	4.2	142	7	US-11-087-099-4976	Sequence 4976, Ap
30	9	4.2	144	6	US-10-821-234-1254	Sequence 1254, Ap
31	9	4.2	146	7	US-11-172-740-1569	Sequence 1569, Ap
32	9	4.2	149	7	US-11-087-099-3510	Sequence 3510, Ap
33	9	4.2	149	7	US-11-172-740-1571	Sequence 1571, Ap
34	9	4.2	152	7	US-11-087-099-313	Sequence 313, App
35	9	4.2	152	7	US-11-172-740-1565	Sequence 1565, Ap
36	9	4.2	152	7	US-11-172-740-1566	Sequence 1566, Ap
37	9	4.2	154	7	US-11-087-099-2474	Sequence 2474, Ap
38	9	4.2	154	7	US-11-172-740-1570	Sequence 1570, Ap
39	9	4.2	159	7	US-11-087-099-9017	Sequence 9017, Ap
40	9	4.2	162	7	US-11-096-568A-9680	Sequence 9680, Ap
41	9	4.2	164	7	US-11-096-568A-3510	Sequence 3510, Ap
42	9	4.2	168	7	US-11-233-510-4	Sequence 4, Appli
43	9	4.2	187	7	US-11-096-568A-26883	Sequence 26883, A
44	9	4.2	245	7	US-11-096-568A-28368	Sequence 28368, A
45	9	4.2	291	6	US-10-501-035-245	Sequence 245, App

ALIGNMENTS

RESULT 1
US-10-821-234-1443
; Sequence 1443, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1443
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1443

Query Match 100.0%; Score 215; DB 6; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.3e-192;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
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RESULT 2
US-11-186-422-11
; Sequence 11, Application US/11186422
; Publication No. US20060057679A1

```
; GENERAL INFORMATION:
;  APPLICANT: Critical Therapeutics, Inc.
;  APPLICANT:  O'Keefe, Theresa
;  APPLICANT:  Luciano, Peter
;  APPLICANT:  Qin, Shixin
;  TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
;  FILE REFERENCE: 3258.1021-003
;  CURRENT APPLICATION NUMBER: US/11/186,422
;  CURRENT FILING DATE:  2005-07-20
;  PRIOR APPLICATION NUMBER: 60/589,678
;  PRIOR FILING DATE: 2004-07-20
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-186-422-11

  Query Match             100.0%;  Score 215;  DB 7;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-192;
  Matches  215;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215
              |||||||||||||||||||||||||||||||||||
Db        181 SKKKKEEEEDEEDEEDEEEEEDEEDEDEEEDDDDE 215


RESULT 3
US-11-186-422-12
; Sequence 12, Application US/11186422
; Publication No. US20060057679A1
; GENERAL INFORMATION:
;  APPLICANT: Critical Therapeutics, Inc.
;  APPLICANT:  O'Keefe, Theresa
;  APPLICANT:  Luciano, Peter
;  APPLICANT:  Qin, Shixin
;  TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
;  FILE REFERENCE: 3258.1021-003
;  CURRENT APPLICATION NUMBER: US/11/186,422
;  CURRENT FILING DATE:  2005-07-20
;  PRIOR APPLICATION NUMBER: 60/589,678
;  PRIOR FILING DATE: 2004-07-20
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-11-186-422-12

  Query Match             87.4%;  Score 188;  DB 7;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-167;
  Matches  188;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGKGDPKKPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF 60

Qy         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDMAKADKARYEREMKTYIPPKGETKKKFKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGL 120

Qy        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAAKKGVVKAEK 180

Qy        181 SKKKKEEE 188
              ||||||||
Db        181 SKKKKEEE 188


RESULT 4
US-11-186-422-14
; Sequence 14, Application US/11186422
; Publication No. US20060057679A1
; GENERAL INFORMATION:
;  APPLICANT: Critical Therapeutics, Inc.
;  APPLICANT:  O'Keefe, Theresa
;  APPLICANT:  Luciano, Peter
;  APPLICANT:  Qin, Shixin
;  TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
;  FILE REFERENCE: 3258.1021-003
;  CURRENT APPLICATION NUMBER: US/11/186,422
;  CURRENT FILING DATE:  2005-07-20
;  PRIOR APPLICATION NUMBER: 60/589,678
;  PRIOR FILING DATE: 2004-07-20
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 69
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-186-422-14

  Query Match             32.1%;  Score 69;  DB 7;  Length 69;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-57;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         93 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60

Qy        153 EKYEKDIAA 161
              |||||||||
Db         61 EKYEKDIAA 69


RESULT 5
US-10-719-150-6
; Sequence 6, Application US/10719150
; Publication No. US20040120953A1
; GENERAL INFORMATION:
;  APPLICANT: Kevin J. Tracey
;  APPLICANT:  Haichao Wang
;  TITLE OF INVENTION: ANTAGONISTS OF HMG1 FOR TREATING
;  TITLE OF INVENTION:  INFLAMMATORY CONDITIONS
;  FILE REFERENCE: 3268.1000-011
;  CURRENT APPLICATION NUMBER: US/10/719,150
;  CURRENT FILING DATE:  2003-11-21
;  PRIOR APPLICATION NUMBER: US/10/300,068
;  PRIOR FILING DATE: 2002-11-20
;  PRIOR APPLICATION NUMBER: US 10/210,747
;  PRIOR FILING DATE: 2002-07-31
;  PRIOR APPLICATION NUMBER: US 09/503,632
;  PRIOR FILING DATE: 2000-02-14
;  PRIOR APPLICATION NUMBER: US 09/248,574
;  PRIOR FILING DATE: 1999-02-11
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 54
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
```

US-10-719-150-6

Query Match 25.1%; Score 54; DB 6; Length 54;
Best Local Similarity 100.0%; Pred. No. 2e-43;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         32 PDASVNFSEFSKKCSERWKTMSAKEKGKFEDMAKADKARYEREMKTYIPPKGET 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 PDASVNFSEFSKKCSERWKTMSAKEKGKFEDMAKADKARYEREMKTYIPPKGET 54
```

RESULT 6
US-11-186-422-13
; Sequence 13, Application US/11186422
; Publication No. US20060057679A1
; GENERAL INFORMATION:
; APPLICANT: Critical Therapeutics, Inc.
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Luciano, Peter
; APPLICANT: Qin, Shixin
; TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
; FILE REFERENCE: 3258.1021-003
; CURRENT APPLICATION NUMBER: US/11/186,422
; CURRENT FILING DATE: 2005-07-20
; PRIOR APPLICATION NUMBER: 60/589,678
; PRIOR FILING DATE: 2004-07-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-186-422-13

Query Match 25.1%; Score 54; DB 7; Length 54;
Best Local Similarity 100.0%; Pred. No. 2e-43;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         32 PDASVNFSEFSKKCSERWKTMSAKEKGKFEDMAKADKARYEREMKTYIPPKGET 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 PDASVNFSEFSKKCSERWKTMSAKEKGKFEDMAKADKARYEREMKTYIPPKGET 54
```

RESULT 7
US-11-169-041-192
; Sequence 192, Application US/11169041
; Publication No. US20060019284A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
; TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
; TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 10001 NP
; CURRENT APPLICATION NUMBER: US/11/169,041
; CURRENT FILING DATE: 2005-06-28
; PRIOR APPLICATION NUMBER: 60/584,405
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 527
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 192
; LENGTH: 879
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-169-041-192

Query Match 10.2%; Score 22; DB 7; Length 879;
Best Local Similarity 100.0%; Pred. No. 1.4e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        101 AFFLFCSEYRPKIKGEHPGLSI 122
              ||||||||||||||||||||||
Db        775 AFFLFCSEYRPKIKGEHPGLSI 796
```

RESULT 8
US-10-821-234-1234
; Sequence 1234, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1234
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(169)
; OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-821-234-1234

Query Match 9.3%; Score 20; DB 6; Length 169;
Best Local Similarity 100.0%; Pred. No. 2.3e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         14 SSYAFFVQTCREEHKKKHPD 33
              ||||||||||||||||||||
Db          1 SSYAFFVQTCREEHKKKHPD 20
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RESULT 9
US-10-719-150-1
; Sequence 1, Application US/10719150
; Publication No. US20040120953A1
; GENERAL INFORMATION:
; APPLICANT: Kevin J. Tracey
; APPLICANT: Haichao Wang
; TITLE OF INVENTION: ANTAGONISTS OF HMG1 FOR TREATING
; TITLE OF INVENTION: INFLAMMATORY CONDITIONS
; FILE REFERENCE: 3268.1000-011
; CURRENT APPLICATION NUMBER: US/10/719,150
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US/10/300,068
; PRIOR FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: US 10/210,747
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 09/503,632
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: US 09/248,574
; PRIOR FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-719-150-1

Query Match 6.5%; Score 14; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.4e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          2 GKGDPKKPRGKMSS 15
              ||||||||||||||
Db          1 GKGDPKKPRGKMSS 14
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```
RESULT 10
US-10-719-150-4
; Sequence 4, Application US/10719150
; Publication No. US20040120953A1
; GENERAL INFORMATION:
;  APPLICANT: Kevin J. Tracey
;  APPLICANT:  Haichao Wang
;  TITLE OF INVENTION: ANTAGONISTS OF HMG1 FOR TREATING
;  TITLE OF INVENTION:  INFLAMMATORY CONDITIONS
;  FILE REFERENCE: 3268.1000-011
;  CURRENT APPLICATION NUMBER: US/10/719,150
;  CURRENT FILING DATE:  2003-11-21
;  PRIOR APPLICATION NUMBER: US/10/300,068
;  PRIOR FILING DATE: 2002-11-20
;  PRIOR APPLICATION NUMBER: US 10/210,747
;  PRIOR FILING DATE: 2002-07-31
;  PRIOR APPLICATION NUMBER: US 09/503,632
;  PRIOR FILING DATE: 2000-02-14
;  PRIOR APPLICATION NUMBER: US 09/248,574
;  PRIOR FILING DATE: 1999-02-11
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antigen
US-10-719-150-4

  Query Match             6.5%;  Score 14;  DB 6;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1e-06;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 GKGDPKKPRGKMSS 15
              ||||||||||||||
Db          1 GKGDPKKPRGKMSS 14


RESULT 11
US-11-044-899-2
; Sequence 2, Application US/11044899
; Publication No. US20050260616A1
; GENERAL INFORMATION:
;  APPLICANT: Schwab, M.
;  APPLICANT:  Chen, M.
;  TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
;  TITLE OF INVENTION:  THEREON
;  FILE REFERENCE: 10200-017-999
;  CURRENT APPLICATION NUMBER: US/11/044,899
;  CURRENT FILING DATE:  2005-01-26
;  PRIOR APPLICATION NUMBER: 09/830,972
;  PRIOR FILING DATE: 2001-09-24
;  PRIOR APPLICATION NUMBER: PCT/US99/26160
;  PRIOR FILING DATE: 1999-11-05
;  PRIOR APPLICATION NUMBER: 60/107,446
;  PRIOR FILING DATE: 1998-11-06
;  NUMBER OF SEQ ID NOS: 51
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 1163
;   TYPE: PRT
;   ORGANISM: Rattus sp.
US-11-044-899-2

  Query Match             6.0%;  Score 13;  DB 7;  Length 1163;
  Best Local Similarity   100.0%;  Pred. No. 0.00042;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        192 EDEEDEEEEEDEE 204
              |||||||||||||
Db         33 EDEEDEEEEEDEE 45


RESULT 12
US-11-044-899-30
; Sequence 30, Application US/11044899
; Publication No. US20050260616A1
; GENERAL INFORMATION:
;  APPLICANT: Schwab, M.
;  APPLICANT:  Chen, M.
;  TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO GENES AND METHODS BASED
;  TITLE OF INVENTION:  THEREON
;  FILE REFERENCE: 10200-017-999
;  CURRENT APPLICATION NUMBER: US/11/044,899
;  CURRENT FILING DATE:  2005-01-26
;  PRIOR APPLICATION NUMBER: 09/830,972
;  PRIOR FILING DATE: 2001-09-24
;  PRIOR APPLICATION NUMBER: PCT/US99/26160
;  PRIOR FILING DATE: 1999-11-05
;  PRIOR APPLICATION NUMBER: 60/107,446
;  PRIOR FILING DATE: 1998-11-06
;  NUMBER OF SEQ ID NOS: 51
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 30
;   LENGTH: 1163
;   TYPE: PRT
;   ORGANISM: Rattus sp.
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(1163) at all Xaa position
;   OTHER INFORMATION: Xaa = any amino acid
US-11-044-899-30

  Query Match             6.0%;  Score 13;  DB 7;  Length 1163;
  Best Local Similarity   100.0%;  Pred. No. 0.00042;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        192 EDEEDEEEEEDEE 204
              |||||||||||||
Db         33 EDEEDEEEEEDEE 45


RESULT 13
US-11-087-099-12397
; Sequence 12397, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
;  CURRENT FILING DATE:  2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 12397
;   LENGTH: 1750
;   TYPE: PRT
;   ORGANISM: Neurospora crassa
US-11-087-099-12397

  Query Match             6.0%;  Score 13;  DB 7;  Length 1750;
  Best Local Similarity   100.0%;  Pred. No. 0.00061;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        196 DEEEEEDEEDEDE 208
              |||||||||||||
Db       1726 DEEEEEDEEDEDE 1738


RESULT 14
US-11-096-568A-28367
; Sequence 28367, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 28367
;   LENGTH: 447
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(447)
;   OTHER INFORMATION: Ceres Seq. ID no. 2715782
US-11-096-568A-28367

  Query Match             5.6%;  Score 12;  DB 7;  Length 447;
  Best Local Similarity   100.0%;  Pred. No. 0.0015;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        190 DEEDEEDEEEEE 201
              ||||||||||||
Db        169 DEEDEEDEEEEE 180


RESULT 15
US-11-096-568A-6675
; Sequence 6675, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 6675
;   LENGTH: 106
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(106)
;   OTHER INFORMATION: Ceres Seq. ID no. 14316260
US-11-096-568A-6675

  Query Match             4.7%;  Score 10;  DB 7;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 0.03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        205 DEDEEEDDDD 214
              ||||||||||
Db         40 DEDEEEDDDD 49


Search completed: April  6, 2006, 10:45:44
Job time : 24 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 10:12:19 ; Search time 83.7533 Seconds
(without alignments)
361.981 Million cell updates/sec

Title: US-10-717-984-5
Perfect score: 370
Sequence: 1 NAPKRPPSAFFLFCSEYRPK.....QPYEKKAAKLKEKYEKDIAA 69

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	370	100.0	69	6	AAE35863	Aae35863 HMG1 B bo
2	370	100.0	69	8	ADO25922	Ado25922 High mobi
3	370	100.0	69	8	ADO71481	Ado71481 Human/mou
4	370	100.0	74	8	ADO25934	Ado25934 High mobi
5	370	100.0	74	8	ADO71527	Ado71527 Human hig
6	370	100.0	74	9	ADY85362	Ady85362 Human hig
7	370	100.0	74	9	ADY85078	Ady85078 Human HMG
8	370	100.0	74	9	ADY85087	Ady85087 Human HMG
9	370	100.0	75	8	ADR45941	Adr45941 Human hig
10	370	100.0	92	8	ADO25962	Ado25962 High mobi
11	370	100.0	92	8	ADO71534	Ado71534 Human hig
12	370	100.0	92	9	ADY85368	Ady85368 Human hig
13	370	100.0	92	9	ADY85084	Ady85084 Human HMG
14	370	100.0	128	3	AAB57179	Aab57179 Human pro
15	370	100.0	168	8	ABM81641	Abm81641 Tumour-as
16	370	100.0	176	6	ADA55380	Ada55380 Human pro
17	370	100.0	214	7	ADD47645	Add47645 Human Pro
18	370	100.0	214	7	ADE60730	Ade60730 Rat Prote
19	370	100.0	214	7	ADE60447	Ade60447 Human Pro
20	370	100.0	214	7	ADE57980	Ade57980 Human Pro
21	370	100.0	214	7	ADE57984	Ade57984 Human Pro
22	370	100.0	214	7	ADE57978	Ade57978 Rat Prote
23	370	100.0	214	7	ADE60732	Ade60732 Human Pro
24	370	100.0	214	7	ADE57982	Ade57982 Rat Prote
25	370	100.0	214	7	ADE60726	Ade60726 Rat Prote
26	370	100.0	214	7	ADE60728	Ade60728 Human Pro
27	370	100.0	214	7	ADE60445	Ade60445 Rat Prote
28	370	100.0	214	8	ADS17580	Ads17580 Amino aci
29	370	100.0	215	5	ABB57220	Abb57220 Mouse isc
30	370	100.0	215	6	ABU07499	Abu07499 Protein d
31	370	100.0	215	6	AAE35859	Aae35859 Human HMG
32	370	100.0	215	6	AAE35860	Aae35860 Mouse and
33	370	100.0	215	7	ADD40789	Add40789 Human HMG
34	370	100.0	215	7	ADD40788	Add40788 Human HMG
35	370	100.0	215	7	ADD47643	Add47643 Rat Prote
36	370	100.0	215	7	ABM85677	Abm85677 Human pro
37	370	100.0	215	8	ADO60491	Ado60491 Human hig
38	370	100.0	215	8	ADO25919	Ado25919 Mouse/rat
39	370	100.0	215	8	ADO25918	Ado25918 Human hig
40	370	100.0	215	8	ADO71478	Ado71478 Mouse/rat
41	370	100.0	215	8	ADO71477	Ado71477 Human hig
42	370	100.0	215	8	ADR45922	Adr45922 Human hig
43	370	100.0	215	8	ADR87104	Adr87104 High Mobi
44	370	100.0	215	8	ABM81508	Abm81508 Tumour-as
45	370	100.0	215	9	ADW81011	Adw81011 Amphoteri

ALIGNMENTS

RESULT 1
AAE35863
ID AAE35863 standard; protein; 69 AA.
XX
AC AAE35863;
XX
DT 17-JUN-2003 (first entry)
XX
DE HMG1 B box.
XX
KW Rat; high mobility group; HMG protein; HMG A box; HMG B box; asthma;
KW inflammatory cytokine; endotoxic shock; rheumatoid arthritis; hepatitis;
KW appendicitis; peptic ulcer; duodenal ulcer; Crohn's disease; meningitis;
KW allergy; immune complex disease; sinusitis; bronchitis; atherosclerosis;
KW emphysema; HIV infection; candidiasis; malaria; filariasis; myocarditis;
KW Hodgkin's disease; neuritis; dermatitis; myocardial ischaemia; diabetes;
KW Alzheimer's disease; Goodpasture's syndrome; graft-versus-host disease;
KW amoebiasis; multiple sclerosis; gout; cerebral infarction; peritonitis;
KW gene therapy; human immunodeficiency virus; mouse; human; HMGB1 protein.
XX
OS Mus sp.
OS Rattus sp.
OS Homo sapiens.
XX
PN WO200292004-A2.
XX
PD 21-NOV-2002.
XX
PF 15-MAY-2002; 2002WO-US015329.
XX
PR 15-MAY-2001; 2001US-0291034P.
XX
PA (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
PA (GEHO) GEN HOSPITAL CORP.
PA (UYPI-) UNIV PITTSBURGH.
XX
PI Tracey KJ, Yang H, Warren HS, Fink MP;
XX
DR WPI; 2003-120594/11.
XX
PT New isolated polypeptide having a vertebrate HMG A box, useful for
PT inhibiting a condition associated with an activated inflammatory cytokine
PT cascade, e.g. endotoxic shock, myocardial infarction, asthma, HIV
PT infection, malaria and diabetes.
XX
PS Disclosure; Fig 12E; 82pp; English.
XX

```
CC   The invention relates to high mobility group (HMG) protein comprising DNA
CC   binding motifs termed HMG A box and HMG B box. HMG A box or a non-
CC   naturally occurring HMG A box inhibits the release of a pro-inflammatory
CC   cytokine from a vertebrate cell. The methods and compositions of the
CC   invention are useful for inhibiting a condition characterised by
CC   activation of an inflammatory cytokine cascade such as endotoxic shock,
CC   rheumatoid arthritis, appendicitis, peptic or duodenal ulcers, Crohn's
CC   disease, peritonitis, hepatitis, asthma, allergy, immune complex disease,
CC   sinusitis, bronchitis, emphysema, HIV infection, candidiasis, malaria,
CC   filariasis, amoebiasis, dermatitis, atherosclerosis, Alzheimer's disease,
CC   myocarditis, myocardial ischaemia, meningitis, multiple sclerosis, gout,
CC   cerebral infarction, neuritis, Goodpasture's syndrome, graft-versus-host
CC   disease, diabetes and Hodgkin's disease. The invention is useful in gene
CC   therapy. The present sequence is HMG1 (also termed as HMGB1) B box found
CC   in human, mouse and rat
XX
SQ   Sequence 69 AA;

  Query Match            100.0%;  Score 370;  DB 6;  Length 69;
  Best Local Similarity  100.0%;  Pred. No. 3.7e-38;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60

Qy         61 EKYEKDIAA 69
              |||||||||
Db         61 EKYEKDIAA 69


RESULT 2
ADO25922
ID   ADO25922 standard; protein; 69 AA.
XX
AC   ADO25922;
XX
DT   26-AUG-2004  (first entry)
XX
DE   High mobility group box 1 (HMG1) B box protein sequence.
XX
KW   cytostatic; gene therapy; vaccine; pharmaceutical composition;
KW   HMGB B box; high mobility group; immune response; immunostimulation;
KW   cancer; human; mouse; rat; high mobility group box 1; HMG1;
KW   cytokine activity; B box.
XX
OS   Mammalia.
XX
PN   WO2004046338-A2.
XX
PD   03-JUN-2004.
XX
PF   19-NOV-2003; 2003WO-US036975.
XX
PR   20-NOV-2002; 2002US-0427848P.
XX
PA   (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
XX
PI   Tracey KJ;
XX
DR   WPI; 2004-420625/39.
XX
PT   New pharmaceutical composition comprises a polypeptide comprising an HMGB
PT   B box or its functional variant, useful for stimulating or increasing an
PT   immune response in an individual or for treating cancer in an individual.
XX
PS   Disclosure; SEQ ID NO 5; 68pp; English.
XX
CC   The invention describes a pharmaceutical composition comprising a
CC   polypeptide comprising an HMGB (high mobility group box) B box or its
CC   functional variant to treat a disease or condition by increasing an
CC   immune response in an individual administered with the pharmaceutical
CC   composition. Also described are: an antibody attached to a polypeptide
CC   comprising an HMGB B box or its functional variant; stimulating or
CC   increasing an immune response in an individual in need of
CC   immunostimulation; and treating cancer in an individual. The composition
CC   is useful for stimulating or increasing an immune response in an
CC   individual in need of immunostimulation or for treating cancer in an
CC   individual. This is the amino acid sequence of human/mouse/rat high
CC   mobility group box 1 (HMG1) B box protein sequence that can be used to
CC   stimulate cytokine activity and increase immune response to assist in
CC   treating disease.
XX
SQ   Sequence 69 AA;

  Query Match            100.0%;  Score 370;  DB 8;  Length 69;
  Best Local Similarity  100.0%;  Pred. No. 3.7e-38;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60

Qy         61 EKYEKDIAA 69
              |||||||||
Db         61 EKYEKDIAA 69


RESULT 3
ADO71481
ID   ADO71481 standard; protein; 69 AA.
XX
AC   ADO71481;
XX
DT   26-AUG-2004  (first entry)
XX
DE   Human/mouse/rat high mobility group box 1 (HMGB1) B box protein.
XX
KW   Human; mouse; high mobility group box 1 B box; HMGB1 B box; HMGB;
KW   HMGB A box; HMGB B box; proinflammatory cytokine; weight loss; obesity;
KW   inflammation; inflammatory cytokine cascade; sepsis; allograft rejection;
KW   rheumatoid arthritis; asthma; lupus; adult respiratory distress syndrome;
KW   chronic obstructive pulmonary disease; psoriasis; pancreatitis;
KW   peritonitis; burn; myocardial ischaemia; organic ischaemia;
KW   reperfusion ischaemia; Behcet's disease; graft-versus-host disease;
KW   Crohn's disease; ulcerative colitis; multiple sclerosis; cachexia; rat.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Rattus sp.
XX
PN   WO2004046345-A2.
XX
PD   03-JUN-2004.
XX
PF   20-NOV-2003; 2003WO-US037507.
XX
PR   20-NOV-2002; 2002US-0427841P.
PR   20-NOV-2002; 2002US-0427846P.
XX
PA   (CRIT-) CRITICAL THERAPEUTICS INC.
XX
PI   Newman W,  O'keefe TL;
XX
DR   WPI; 2004-420628/39.
XX
PT   New high mobility group box proteins, useful in treating obesity, sepsis,
PT   rheumatoid arthritis, asthma, psoriasis, burns, myocardial ischemia,
PT   Behcet's disease, ulcerative colitis, multiple sclerosis, or cachexia.
XX
PS   Claim 32; SEQ ID NO 5; 113pp; English.
XX
CC   The invention relates to a polypeptide comprising a high mobility group
CC   box protein (HMGB) A or B box. The HMGB A or B box can inhibit release of
CC   a proinflammatory cytokine from a cell treated with an HMGB protein. The
CC   invention also relates to a purified preparation of antibodies that
```

CC specifically bind to the HMGB B box but do not specifically bind to non-B
CC box epitopes of HMGB, where the antibodies can inhibit release of a
CC proinflammatory cytokine from a cell treated with HMGB, a method for
CC effecting weight loss or treating obesity in a patient, a method of
CC determining whether a compound inhibits inflammation, a pharmaceutical
CC composition comprising an HMGB protein or an antibody that binds to the
CC protein, an agent that inhibits TNF biological activity and a method of
CC treating a condition in a patient characterised by activation of an
CC inflammatory cytokine cascade. Effecting weight loss or treating obesity
CC in a patient comprises administering to the patient an amount of the
CC polypeptide. The polypeptide, antibodies, composition and methods are
CC useful in treating obesity and conditions characterised by activation of
CC an inflammatory cytokine cascade, e.g. sepsis, allograft rejection,
CC rheumatoid arthritis, asthma, lupus, adult respiratory distress syndrome,
CC chronic obstructive pulmonary disease, psoriasis, pancreatitis,
CC peritonitis, burns, myocardial ischaemia, organic ischaemia, reperfusion
CC ischaemia, Behcet's disease, graft-versus-host disease, Crohn's disease,
CC ulcerative colitis, multiple sclerosis or cachexia. This sequence
CC represents a human/mouse/rat HMGB1 B box polypeptide of the invention.
XX
SQ Sequence 69 AA;

Query Match 100.0%; Score 370; DB 8; Length 69;
Best Local Similarity 100.0%; Pred. No. 3.7e-38;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60

Qy 61 EKYEKDIAA 69
|||||||||
Db 61 EKYEKDIAA 69

RESULT 4
ADO25934
ID ADO25934 standard; peptide; 74 AA.
XX
AC ADO25934;
XX
DT 26-AUG-2004 (first entry)
XX
DE High mobility group box 1 B box fragment seqid 17.
XX
KW cytostatic; gene therapy; vaccine; pharmaceutical composition;
KW HMGB B box; high mobility group; immune response; immunostimulation;
KW cancer; human; high mobility group box 1; HMG1; cytokine activity; B box.
XX
OS Homo sapiens.
XX
PN WO2004046338-A2.
XX
PD 03-JUN-2004.
XX
PF 19-NOV-2003; 2003WO-US036975.
XX
PR 20-NOV-2002; 2002US-0427848P.
XX
PA (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
XX
PI Tracey KJ;
XX
DR WPI; 2004-420625/39.
XX
PT New pharmaceutical composition comprises a polypeptide comprising an HMGB
PT B box or its functional variant, useful for stimulating or increasing an
PT immune response in an individual or for treating cancer in an individual.
XX
PS Disclosure; SEQ ID NO 17; 68pp; English.
XX
CC The invention describes a pharmaceutical composition comprising a
CC polypeptide comprising an HMGB (high mobility group box) B box or its
CC functional variant to treat a disease or condition by increasing an
CC immune response in an individual administered with the pharmaceutical
CC composition. Also described are: an antibody attached to a polypeptide
CC comprising an HMGB B box or its functional variant; stimulating or
CC increasing an immune response in an individual in need of
CC immunostimulation; and treating cancer in an individual. The composition
CC is useful for stimulating or increasing an immune response in an
CC individual in need of immunostimulation or for treating cancer in an
CC individual. This is the amino acid sequence of human high mobility group
CC box 1 (HMG1) B box biologically active fragment.
XX
SQ Sequence 74 AA;

Query Match 100.0%; Score 370; DB 8; Length 74;
Best Local Similarity 100.0%; Pred. No. 4e-38;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 64

Qy 61 EKYEKDIAA 69
|||||||||
Db 65 EKYEKDIAA 73

RESULT 5
ADO71527
ID ADO71527 standard; protein; 74 AA.
XX
AC ADO71527;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human high mobility group box (HMGB) B box protein #1.
XX
KW Human; high mobility group box B box; HMGB; HMGB A box; HMGB B box;
KW proinflammatory cytokine; weight loss; obesity; inflammation;
KW inflammatory cytokine cascade; sepsis; allograft rejection;
KW rheumatoid arthritis; asthma; lupus; adult respiratory distress syndrome;
KW chronic obstructive pulmonary disease; psoriasis; pancreatitis;
KW peritonitis; burn; myocardial ischaemia; organic ischaemia;
KW reperfusion ischaemia; Behcet's disease; graft-versus-host disease;
KW Crohn's disease; ulcerative colitis; multiple sclerosis; cachexia.
XX
OS Homo sapiens.
XX
PN WO2004046345-A2.
XX
PD 03-JUN-2004.
XX
PF 20-NOV-2003; 2003WO-US037507.
XX
PR 20-NOV-2002; 2002US-0427841P.
PR 20-NOV-2002; 2002US-0427846P.
XX
PA (CRIT-) CRITICAL THERAPEUTICS INC.
XX
PI Newman W, O'keefe TL;
XX
DR WPI; 2004-420628/39.
XX
PT New high mobility group box proteins, useful in treating obesity, sepsis,
PT rheumatoid arthritis, asthma, psoriasis, burns, myocardial ischemia,
PT Behcet's disease, ulcerative colitis, multiple sclerosis, or cachexia.
XX
PS Disclosure; SEQ ID NO 51; 113pp; English.
XX
CC The invention relates to a polypeptide comprising a high mobility group
CC box protein (HMGB) A or B box. The HMGB A or B box can inhibit release of
CC a proinflammatory cytokine from a cell treated with an HMGB protein. The
CC invention also relates to a purified preparation of antibodies that
CC specifically bind to the HMGB B box but do not specifically bind to non-B

```
CC   box epitopes of HMGB, where the antibodies can inhibit release of a
CC   proinflammatory cytokine from a cell treated with HMGB, a method for
CC   effecting weight loss or treating obesity in a patient, a method of
CC   determining whether a compound inhibits inflammation, a pharmaceutical
CC   composition comprising an HMGB protein or an antibody that binds to the
CC   protein, an agent that inhibits TNF biological activity and a method of
CC   treating a condition in a patient characterised by activation of an
CC   inflammatory cytokine cascade. Effecting weight loss or treating obesity
CC   in a patient comprises administering to the patient an amount of the
CC   polypeptide. The polypeptide, antibodies, composition and methods are
CC   useful in treating obesity and conditions characterised by activation of
CC   an inflammatory cytokine cascade, e.g. sepsis, allograft rejection,
CC   rheumatoid arthritis, asthma, lupus, adult respiratory distress syndrome,
CC   chronic obstructive pulmonary disease, psoriasis, pancreatitis,
CC   peritonitis, burns, myocardial ischaemia, organic ischaemia, reperfusion
CC   ischaemia, Behcet's disease, graft-versus-host disease, Crohn's disease,
CC   ulcerative colitis, multiple sclerosis or cachexia. This sequence
CC   represents a human HMGB B box polypeptide of the invention.
XX
SQ   Sequence 74 AA;

  Query Match             100.0%;  Score 370;  DB 8;  Length 74;
  Best Local Similarity   100.0%;  Pred. No. 4e-38;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 64

Qy         61 EKYEKDIAA 69
              |||||||||
Db         65 EKYEKDIAA 73


RESULT 6
ADY85362
ID   ADY85362 standard; protein; 74 AA.
XX
AC   ADY85362;
XX
DT   02-JUN-2005  (first entry)
XX
DE   Human high mobility group box protein HMGB1 B box.
XX
KW   High mobility group box; HMGB1; immune disorder; infection;
KW   immunosuppressive; autoimmune disease; allergy; antiallergic;
KW   ulcerative colitis; antiinflammatory; antiulcer; gastrointestinal-gen.;
KW   Crohns disease; inflammation; asthma; antiasthmatic;
KW   rheumatoid arthritis; antirheumatic; antiarthritic; psoriasis;
KW   antipsoriatic; systemic lupus erythematosus; dermatological; antiulcer.
XX
OS   Homo sapiens.
XX
PN   WO2005025604-A2.
XX
PD   24-MAR-2005.
XX
PF   10-SEP-2004; 2004WO-US029540.
XX
PR   10-SEP-2003; 2003US-0502349P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
XX
PI   Warren HS,  Tracey KJ;
XX
DR   WPI; 2005-233421/24.
XX
PT   Treating an immune pathology in an individual comprises administering an
PT   amount of a high mobility group box (HMGB) polypeptide comprising a
PT   vertebrate or a non-naturally occurring HMGB A or B box, or its
PT   immunosuppressive fragment.
XX
PS   Disclosure; SEQ ID NO 37; 57pp; English.
XX
CC   The invention is based on the discovery that high mobility group box
CC   protein 1 (HMGB1, also known as high mobility group-1 or HMG1), when
CC   administered with an antigen, diminishes the antibody response to the
CC   administered antigen. HMGB1 has 2 DNA binding motifs, termed the A and B
CC   boxes. A claimed method of treating an immune pathology in an individual
CC   comprises administering a HMGB polypeptide comprising a vertebrate HMGB A
CC   box, a non-naturally-occurring HMGB A box, or an immunosuppressive
CC   fragment of the vertebrate or non-natural HMGB A box. The immune
CC   pathology is induced by the administration of a non-human antigen, non-
CC   self material (e.g. a cell or tissue such as bone marrow cells) or
CC   adjuvant to the individual, by the transplantation of an organ into the
CC   individual, or by infection from a microorganism. Claimed methods of
CC   protecting a subject against an immune pathology, inhibiting an immune
CC   pathology in an individual or decreasing an immune response to an
CC   administered non-human antigen comprise administering a HMGB polypeptide
CC   comprising a vertebrate HMGB A box, a non-naturally-occurring HMGB A box,
CC   or an immunosuppressive fragment of the vertebrate or non-natural A box.
CC   A claimed method of treating an autoimmune disorder in an individual
CC   comprises administering a HMGB polypeptide comprising a vertebrate HMGB A
CC   box, a non-naturally-occurring HMGB A box, or an immunosuppressive
CC   fragment of these, and a vertebrate or non-naturally-occurring HMGB B
CC   box. The HMGB polypeptide is preferably a HMGB1 peptide and may be
CC   truncated at the C-terminus. The autoimmune disease is allergy,
CC   ulcerative colitis, Crohn's disease, asthma, rheumatoid arthritis,
CC   psoriasis or systemic lupus erythematosus (all claimed). The present
CC   sequence is that of the B box of human HMGB1 protein ADY85326.
XX
SQ   Sequence 74 AA;

  Query Match             100.0%;  Score 370;  DB 9;  Length 74;
  Best Local Similarity   100.0%;  Pred. No. 4e-38;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 64

Qy         61 EKYEKDIAA 69
              |||||||||
Db         65 EKYEKDIAA 73


RESULT 7
ADY85078
ID   ADY85078 standard; protein; 74 AA.
XX
AC   ADY85078;
XX
DT   16-JUN-2005  (first entry)
XX
DE   Human HMGB1 A box.
XX
KW   High mobility group box; HMGB1; monoclonal antibody; antibody therapy;
KW   sepsis; antibacterial immunosuppressive; graft rejection; arthritis;
KW   antiarthritic; asthma; antiasthmatic; lupus erythematosus;
KW   antiinflammatory; inflammation; dermatological;
KW   respiratory distress syndrome; respiratory-gen.; psoriasis;
KW   antipsoriatic; chronic obstructive pulmonary disease; pancreatitis;
KW   peritonitis; burns; vulnerary; ischemia; vasotropic; Behcets disease;
KW   graft versus host disease; inflammatory bowel disease;
KW   gastrointestinal-gen.; multiple sclerosis neuroprotective; cachexia;
KW   anabolic; infection; musculoskeletal disease; immune disorder.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Rattus sp.
XX
PN   WO2005026209-A2.
XX
PD   24-MAR-2005.
XX
```

PF 10-SEP-2004; 2004WO-US029527.
XX
PR 11-SEP-2003; 2003US-0502568P.
XX
PA (CRIT-) CRITICAL THERAPEUTICS INC.
XX
PI Newman W, Qin S, Okeefe T, Obar R;
XX
DR WPI; 2005-233483/24.
XX
PT New antibody or its antigen-binding fragment specific to a vertebrate
PT high mobility group box (HMGB) A box that inhibits release of a
PT proinflammatory cytokine from a cell treated with HMGB protein, useful
PT for treating, e.g. sepsis.
XX
PS Disclosure; SEQ ID NO 2; 123pp; English.
XX
CC The invention provides antibodies, or their antigen-binding fragments,
CC that bind to a vertebrate high mobility group box (HMGB) polypeptide, to
CC methods of detecting and/or identifying an agent that binds to an HMGB
CC polypeptide, methods of treating a condition in a subject characterized
CC by activation of an inflammatory cytokine cascade, and methods of
CC detecting an HMGB polypeptide in a sample. The antibody (or antigen-
CC binding fragment) binds to a vertebrate HMGB A box but does not
CC specifically bind to non-A box epitopes of HMGB, and inhibits release of
CC a proinflammatory cytokine from a vertebrate cell treated with an HMGB
CC protein. A method of treating a condition characterized by activation of
CC an inflammatory cytokine cascade comprises administering an antibody of
CC the invention, or its antigen-binding fragment. The condition is selected
CC from sepsis, allograft rejection, arthritis, asthma, lupus, adult
CC respiratory distress syndrome, chronic obstructive pulmonary disease,
CC psoriasis, pancreatitis, peritonitis, burns, ischemia, Behcet's disease,
CC graft versus host disease, inflammatory bowel disease, multiple sclerosis
CC and cachexia, especially sepsis, arthritis, or lupus. The present
CC sequence is that of the A box of human HMGB1 ADY85012. An identical
CC sequence is also found in rat and mouse HMGB1.
XX
SQ Sequence 74 AA;

Query Match 100.0%; Score 370; DB 9; Length 74;
Best Local Similarity 100.0%; Pred. No. 4e-38;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 64

Qy 61 EKYEKDIAA 69
|||||||||
Db 65 EKYEKDIAA 73

RESULT 8
ADY85087
ID ADY85087 standard; protein; 74 AA.
XX
AC ADY85087;
XX
DT 16-JUN-2005 (first entry)
XX
DE Human HMGB1 A box.
XX
KW High mobility group box; HMGB1; monoclonal antibody; antibody therapy;
KW sepsis; antibacterial immunosuppressive; graft rejection; arthritis;
KW antiarthritic; asthma; antiasthmatic; lupus erythematosus;
KW antiinflammatory; inflammation; dermatological;
KW respiratory distress syndrome; respiratory-gen.; psoriasis;
KW antipsoriatic; chronic obstructive pulmonary disease; pancreatitis;
KW peritonitis; burns; vulnerary; ischemia; vasotropic; Behcets disease;
KW graft versus host disease; inflammatory bowel disease;
KW gastrointestinal-gen.; multiple sclerosis neuroprotective; cachexia;
KW anabolic; infection; musculoskeletal disease; immune disorder.
XX
OS Homo sapiens.
OS Mus sp.
OS Rattus sp.
XX
PN WO2005026209-A2.
XX
PD 24-MAR-2005.
XX
PF 10-SEP-2004; 2004WO-US029527.
XX
PR 11-SEP-2003; 2003US-0502568P.
XX
PA (CRIT-) CRITICAL THERAPEUTICS INC.
XX
PI Newman W, Qin S, Okeefe T, Obar R;
XX
DR WPI; 2005-233483/24.
XX
PT New antibody or its antigen-binding fragment specific to a vertebrate
PT high mobility group box (HMGB) A box that inhibits release of a
PT proinflammatory cytokine from a cell treated with HMGB protein, useful
PT for treating, e.g. sepsis.
XX
PS Disclosure; SEQ ID NO 2; 123pp; English.
XX
CC The invention provides antibodies, or their antigen-binding fragments,
CC that bind to a vertebrate high mobility group box (HMGB) polypeptide, to
CC methods of detecting and/or identifying an agent that binds to an HMGB
CC polypeptide, methods of treating a condition in a subject characterized
CC by activation of an inflammatory cytokine cascade, and methods of
CC detecting an HMGB polypeptide in a sample. The antibody (or antigen-
CC binding fragment) binds to a vertebrate HMGB A box but does not
CC specifically bind to non-A box epitopes of HMGB, and inhibits release of
CC a proinflammatory cytokine from a vertebrate cell treated with an HMGB
CC protein. A method of treating a condition characterized by activation of
CC an inflammatory cytokine cascade comprises administering an antibody of
CC the invention, or its antigen-binding fragment. The condition is selected
CC from sepsis, allograft rejection, arthritis, asthma, lupus, adult
CC respiratory distress syndrome, chronic obstructive pulmonary disease,
CC psoriasis, pancreatitis, peritonitis, burns, ischemia, Behcet's disease,
CC graft versus host disease, inflammatory bowel disease, multiple sclerosis
CC and cachexia, especially sepsis, arthritis, or lupus. The present
CC sequence is that of the A box of human HMGB1 ADY85012. An identical
CC sequence is also found in rat and mouse HMGB1.
XX
SQ Sequence 74 AA;

Query Match 100.0%; Score 370; DB 9; Length 74;
Best Local Similarity 100.0%; Pred. No. 4e-38;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 64

Qy 61 EKYEKDIAA 69
|||||||||
Db 65 EKYEKDIAA 73

RESULT 9
ADR45941
ID ADR45941 standard; protein; 75 AA.
XX
AC ADR45941;
XX
DT 21-OCT-2004 (first entry)
XX
DE Human high mobility group HMGB1 HMG-BOXB(large) protein.
XX
KW antidiabetic; ophthalmological; nephropathic; antiarthritic;
KW antiinflammatory; cytostatic; gynaecological; antipsoriatic;
KW dermatological; antiviral; vasotropic; antiarteriosclerotic; antianginal;

KW cardiant; vulnerary; antiulcer; high mobility group protein; human.
XX
OS Homo sapiens.
XX
PN WO2004061456-A2.
XX
PD 22-JUL-2004.
XX
PF 05-JAN-2004; 2004WO-EP000030.
XX
PR 03-JAN-2003; 2003DE-01000023.
PR 07-MAR-2003; 2003DE-01010160.
PR 10-AUG-2003; 2003DE-01036642.
PR 08-OCT-2003; 2003DE-01046614.
XX
PA (ALCE-) ALCEDO BIOTECH GMBH.
XX
PI Bullerdiek J;
XX
DR WPI; 2004-571355/55.
DR N-PSDB; ADR45975.
XX
PT Use of nucleic acids encoding basic DNA-binding proteins, and their
PT translation or transcription products, for treating diseases associated
PT with e.g. angiogenesis, neovascularization or wound healing, also for
PT drug screening.
XX
PS Claim 57; SEQ ID NO 26; 161pp; German.
XX
CC The present invention relates to the use, especially in vitro, of nucleic
CC acids encoding high mobility group proteins for the following processes:
CC angiogenesis (including in a wound bed), neovascularization,
CC transmyocardial revascularization, wound healing, epithelialization and
CC healing in cases of tooth or bone implants. The sequences and their
CC encoded protein are useful for treating a very wide range of diseases:
CC (proliferative) diabetic retinopathy, diabetic nephropathy, macular
CC degeneration, arthritis, endometriosis, histiocytosis, psoriasis,
CC rosacea, eruptive or cavernous haemangioma, tumours (especially melanoma,
CC Kaposi sarcoma and basal cell carcinoma), haemorrhoids, arteriosclerosis,
CC angina pectoris, ischaemia, infarction, infertility, wounds (including
CC diabetic and other ulcers), also diseases associated with DNA damage,
CC especially xeroderma pigmentosum, 'leather skin', skin cancers and ageing
CC (including where associated with sunburn) and cardiac infarct, including
CC cosmetic treatment, especially as a sun-protection composition. Compounds
CC identified as modulators of the specified processes can also be used
CC therapeutically. The present sequence is a polypeptide of the invention.
XX
SQ Sequence 75 AA;

Query Match 100.0%; Score 370; DB 8; Length 75;
Best Local Similarity 100.0%; Pred. No. 4.1e-38;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
Db 2 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 61

Qy 61 EKYEKDIAA 69
Db 62 EKYEKDIAA 70

RESULT 10
ADO25962
ID ADO25962 standard; peptide; 92 AA.
XX
AC ADO25962;
XX
DT 26-AUG-2004 (first entry)
XX
DE High mobility group box 1 B box fragment seqid 45.
XX
KW cytostatic; gene therapy; vaccine; pharmaceutical composition;
KW HMGB B box; high mobility group; immune response; immunostimulation;
KW cancer; human; high mobility group box 1; HMG1; cytokine activity; B box.
XX
OS Homo sapiens.
XX
PN WO2004046338-A2.
XX
PD 03-JUN-2004.
XX
PF 19-NOV-2003; 2003WO-US036975.
XX
PR 20-NOV-2002; 2002US-0427848P.
XX
PA (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
XX
PI Tracey KJ;
XX
DR WPI; 2004-420625/39.
XX
PT New pharmaceutical composition comprises a polypeptide comprising an HMGB
PT B box or its functional variant, useful for stimulating or increasing an
PT immune response in an individual or for treating cancer in an individual.
XX
PS Disclosure; SEQ ID NO 45; 68pp; English.
XX
CC The invention describes a pharmaceutical composition comprising a
CC polypeptide comprising an HMGB (high mobility group box) B box or its
CC functional variant to treat a disease or condition by increasing an
CC immune response in an individual administered with the pharmaceutical
CC composition. Also described are: an antibody attached to a polypeptide
CC comprising an HMGB B box or its functional variant; stimulating or
CC increasing an immune response in an individual in need of
CC immunostimulation; and treating cancer in an individual. The composition
CC is useful for stimulating or increasing an immune response in an
CC individual in need of immunostimulation or for treating cancer in an
CC individual. This is the amino acid sequence of human high mobility group
CC box 1 (HMG1) B box biologically active fragment.
XX
SQ Sequence 92 AA;

Query Match 100.0%; Score 370; DB 8; Length 92;
Best Local Similarity 100.0%; Pred. No. 5.1e-38;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
Db 5 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 64

Qy 61 EKYEKDIAA 69
Db 65 EKYEKDIAA 73

RESULT 11
ADO71534
ID ADO71534 standard; protein; 92 AA.
XX
AC ADO71534;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human high mobility group box (HMGB) B box protein #7.
XX
KW Human; high mobility group box B box; HMGB; HMGB A box; HMGB B box;
KW proinflammatory cytokine; weight loss; obesity; inflammation;
KW inflammatory cytokine cascade; sepsis; allograft rejection;
KW rheumatoid arthritis; asthma; lupus; adult respiratory distress syndrome;
KW chronic obstructive pulmonary disease; psoriasis; pancreatitis;
KW peritonitis; burn; myocardial ischaemia; organic ischaemia;
KW reperfusion ischaemia; Behcet's disease; graft-versus-host disease;
KW Crohn's disease; ulcerative colitis; multiple sclerosis; cachexia.
XX
OS Homo sapiens.

XX
PN WO2004046345-A2.
XX
PD 03-JUN-2004.
XX
PF 20-NOV-2003; 2003WO-US037507.
XX
PR 20-NOV-2002; 2002US-0427841P.
PR 20-NOV-2002; 2002US-0427846P.
XX
PA (CRIT-) CRITICAL THERAPEUTICS INC.
XX
PI Newman W, O'keefe TL;
XX
DR WPI; 2004-420628/39.
XX
PT New high mobility group box proteins, useful in treating obesity, sepsis,
PT rheumatoid arthritis, asthma, psoriasis, burns, myocardial ischemia,
PT Behcet's disease, ulcerative colitis, multiple sclerosis, or cachexia.
XX
PS Disclosure; SEQ ID NO 58; 113pp; English.
XX
CC The invention relates to a polypeptide comprising a high mobility group
CC box protein (HMGB) A or B box. The HMGB A or B box can inhibit release of
CC a proinflammatory cytokine from a cell treated with an HMGB protein. The
CC invention also relates to a purified preparation of antibodies that
CC specifically bind to the HMGB B box but do not specifically bind to non-B
CC box epitopes of HMGB, where the antibodies can inhibit release of a
CC proinflammatory cytokine from a cell treated with HMGB, a method for
CC effecting weight loss or treating obesity in a patient, a method of
CC determining whether a compound inhibits inflammation, a pharmaceutical
CC composition comprising an HMGB protein or an antibody that binds to the
CC protein, an agent that inhibits TNF biological activity and a method of
CC treating a condition in a patient characterised by activation of an
CC inflammatory cytokine cascade. Effecting weight loss or treating obesity
CC in a patient comprises administering to the patient an amount of the
CC polypeptide. The polypeptide, antibodies, composition and methods are
CC useful in treating obesity and conditions characterised by activation of
CC an inflammatory cytokine cascade, e.g. sepsis, allograft rejection,
CC rheumatoid arthritis, asthma, lupus, adult respiratory distress syndrome,
CC chronic obstructive pulmonary disease, psoriasis, pancreatitis,
CC peritonitis, burns, myocardial ischaemia, organic ischaemia, reperfusion
CC ischaemia, Behcet's disease, graft-versus-host disease, Crohn's disease,
CC ulcerative colitis, multiple sclerosis or cachexia. This sequence
CC represents a human HMGB B box polypeptide of the invention.
XX
SQ Sequence 92 AA;

Query Match 100.0%; Score 370; DB 8; Length 92;
Best Local Similarity 100.0%; Pred. No. 5.1e-38;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 64

Qy 61 EKYEKDIAA 69
|||||||||
Db 65 EKYEKDIAA 73

RESULT 12
ADY85368
ID ADY85368 standard; protein; 92 AA.
XX
AC ADY85368;
XX
DT 02-JUN-2005 (first entry)
XX
DE Human high mobility group box protein HMGB1 B box.
XX
KW High mobility group box; HMGB1; immune disorder; infection;
KW immunosuppressive; autoimmune disease; allergy; antiallergic;
KW ulcerative colitis; antiinflammatory; antiulcer; gastrointestinal-gen.;
KW Crohns disease; inflammation; asthma; antiasthmatic;
KW rheumatoid arthritis; antirheumatic; antiarthritic; psoriasis;
KW antipsoriatic; systemic lupus erythematosus; dermatological; antiulcer.
XX
OS Homo sapiens.
XX
PN WO2005025604-A2.
XX
PD 24-MAR-2005.
XX
PF 10-SEP-2004; 2004WO-US029540.
XX
PR 10-SEP-2003; 2003US-0502349P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
XX
PI Warren HS, Tracey KJ;
XX
DR WPI; 2005-233421/24.
XX
PT Treating an immune pathology in an individual comprises administering an
PT amount of a high mobility group box (HMGB) polypeptide comprising a
PT vertebrate or a non-naturally occurring HMGB A or B box, or its
PT immunosuppressive fragment.
XX
PS Disclosure; SEQ ID NO 43; 57pp; English.
XX
CC The invention is based on the discovery that high mobility group box
CC protein 1 (HMGB1, also known as high mobility group-1 or HMG1), when
CC administered with an antigen, diminishes the antibody response to the
CC administered antigen. HMGB1 has 2 DNA binding motifs, termed the A and B
CC boxes. A claimed method of treating an immune pathology in an individual
CC comprises administering a HMGB polypeptide comprising a vertebrate HMGB A
CC box, a non-naturally-occurring HMGB A box, or an immunosuppressive
CC fragment of the vertebrate or non-natural HMGB A box. The immune
CC pathology is induced by the administration of a non-human antigen, non-
CC self material (e.g. a cell or tissue such as bone marrow cells) or
CC adjuvant to the individual, by the transplantation of an organ into the
CC individual, or by infection from a microorganism. Claimed methods of
CC protecting a subject against an immune pathology, inhibiting an immune
CC pathology in an individual or decreasing an immune response to an
CC administered non-human antigen comprise administering a HMGB polypeptide
CC comprising a vertebrate HMGB A box, a non-naturally-occurring HMGB A box,
CC or an immunosuppressive fragment of the vertebrate or non-natural A box.
CC A claimed method of treating an autoimmune disorder in an individual
CC comprises administering a HMGB polypeptide comprising a vertebrate HMGB A
CC box, a non-naturally-occurring HMGB A box, or an immunosuppressive
CC fragment of these, and a vertebrate or non-naturally-occurring HMGB B
CC box. The HMGB polypeptide is preferably a HMGB1 peptide and may be
CC truncated at the C-terminus. The autoimmune disease is allergy,
CC ulcerative colitis, Crohn's disease, asthma, rheumatoid arthritis,
CC psoriasis or systemic lupus erythematosus (all claimed). The present
CC sequence is that of the B box of human HMGB1 protein.
XX
SQ Sequence 92 AA;

Query Match 100.0%; Score 370; DB 9; Length 92;
Best Local Similarity 100.0%; Pred. No. 5.1e-38;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 64

Qy 61 EKYEKDIAA 69
|||||||||
Db 65 EKYEKDIAA 73

RESULT 13
ADY85084

```
ID   ADY85084 standard; protein; 92 AA.
XX
AC   ADY85084;
XX
DT   16-JUN-2005  (first entry)
XX
DE   Human HMGB1 A box.
XX
KW   High mobility group box; HMGB1; monoclonal antibody; antibody therapy;
KW   sepsis; antibacterial immunosuppressive; graft rejection; arthritis;
KW   antiarthritic; asthma; antiasthmatic; lupus erythematosus;
KW   antiinflammatory; inflammation; dermatological;
KW   respiratory distress syndrome; respiratory-gen.; psoriasis;
KW   antipsoriatic; chronic obstructive pulmonary disease; pancreatitis;
KW   peritonitis; burns; vulnerary; ischemia; vasotropic; Behcets disease;
KW   graft versus host disease; inflammatory bowel disease;
KW   gastrointestinal-gen.; multiple sclerosis neuroprotective; cachexia;
KW   anabolic; infection; musculoskeletal disease; immune disorder.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Rattus sp.
XX
PN   WO2005026209-A2.
XX
PD   24-MAR-2005.
XX
PF   10-SEP-2004; 2004WO-US029527.
XX
PR   11-SEP-2003; 2003US-0502568P.
XX
PA   (CRIT-) CRITICAL THERAPEUTICS INC.
XX
PI   Newman W,  Qin S,  Okeefe T,  Obar R;
XX
DR   WPI; 2005-233483/24.
XX
PT   New antibody or its antigen-binding fragment specific to a vertebrate
PT   high mobility group box (HMGB) A box that inhibits release of a
PT   proinflammatory cytokine from a cell treated with HMGB protein, useful
PT   for treating, e.g. sepsis.
XX
PS   Disclosure; SEQ ID NO 2; 123pp; English.
XX
CC   The invention provides antibodies, or their antigen-binding fragments,
CC   that bind to a vertebrate high mobility group box (HMGB) polypeptide, to
CC   methods of detecting and/or identifying an agent that binds to an HMGB
CC   polypeptide, methods of treating a condition in a subject characterized
CC   by activation of an inflammatory cytokine cascade, and methods of
CC   detecting an HMGB polypeptide in a sample. The antibody (or antigen-
CC   binding fragment) binds to a vertebrate HMGB A box but does not
CC   specifically bind to non-A box epitopes of HMGB, and inhibits release of
CC   a proinflammatory cytokine from a vertebrate cell treated with an HMGB
CC   protein. A method of treating a condition characterized by activation of
CC   an inflammatory cytokine cascade comprises administering an antibody of
CC   the invention, or its antigen-binding fragment. The condition is selected
CC   from sepsis, allograft rejection, arthritis, asthma, lupus, adult
CC   respiratory distress syndrome, chronic obstructive pulmonary disease,
CC   psoriasis, pancreatitis, peritonitis, burns, ischemia, Behcet's disease,
CC   graft versus host disease, inflammatory bowel disease, multiple sclerosis
CC   and cachexia, especially sepsis, arthritis, or lupus. The present
CC   sequence is that of the A box of human HMGB1 ADY85012. An identical
CC   sequence is also found in rat and mouse HMGB1.
XX
SQ   Sequence 92 AA;

  Query Match            100.0%;  Score 370;  DB 9;  Length 92;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-38;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 64

Qy         61 EKYEKDIAA 69
              |||||||||
Db         65 EKYEKDIAA 73


RESULT 14
AAB57179
ID   AAB57179 standard; protein; 128 AA.
XX
AC   AAB57179;
XX
DT   13-MAR-2001  (first entry)
XX
DE   Human prostate cancer antigen protein sequence SEQ ID NO:1757.
XX
KW   Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
KW   neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
KW   vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological;
KW   antibacterial; gene therapy; neural; immune; reproductive; renal;
KW   gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW   wound; infectious disease.
XX
OS   Homo sapiens.
XX
PN   WO200055174-A1.
XX
PD   21-SEP-2000.
XX
PF   08-MAR-2000; 2000WO-US005988.
XX
PR   12-MAR-1999;   99US-0124270P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
PA   (ROSE/) ROSEN C A.
XX
PI   Rosen CA,  Ruben SM;
XX
DR   WPI; 2000-587513/55.
DR   N-PSDB; AAF16382.
XX
PT   Prostate cancer associated gene sequences, referred to as prostate cancer
PT   antigens, useful for treatment, prevention, and diagnosis of disorders
PT   such as prostate cancer.
XX
PS   Claim 11; Page 2225-2226; 2338pp; English.
XX
CC   AAF15566 to AAF16505 encode the human prostate cancer associated
CC   proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
CC   The prostate cancer antigens can have neuroprotective, cytostatic,
CC   cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal,
CC   nephrotropic, antiinfective, gynaecological and antibacterial activities,
CC   and can be used in gene therapy. The prostate cancer antigen
CC   polynucleotides may be used for detection of prostate cancer, chromosome
CC   identification, as chromosome markers, and for numerous other diagnostic
CC   or research purposes. The prostate cancer antigens may be used to treat
CC   disorders such as neural, immune, muscular, reproductive,
CC   gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC   disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
CC   AAB57303 represent sequences used in the exemplification of the present
CC   invention
XX
SQ   Sequence 128 AA;

  Query Match            100.0%;  Score 370;  DB 3;  Length 128;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-38;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 69

Qy         61 EKYEKDIAA 69
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```
                 |||||||||
Db         70 EKYEKDIAA 78


RESULT 15
ABM81641
ID   ABM81641 standard; protein; 168 AA.
XX
AC   ABM81641;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Tumour-associated antigenic target (TAT) polypeptide PRO82460, SEQ:4238.
XX
KW   Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW   tumour; diagnosis; cell proliferative disorder; breast cancer;
KW   colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW   central nervous system cancer; bladder cancer; pancreatic cancer;
KW   cervical cancer; melanoma; leukaemia; hybridisation probe;
KW   chromosome identification; chromosome mapping; gene mapping;
KW   gene therapy; cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO2004030615-A2.
XX
PD   15-APR-2004.
XX
PF   29-SEP-2003; 2003WO-US028547.
XX
PR   02-OCT-2002; 2002US-0414971P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Wu TD,  Zhang Z,  Zhou Y;
XX
DR   WPI; 2004-347921/32.
DR   N-PSDB; ACN39840.
XX
PT   New tumor-associated antigenic target polypeptides and nucleic acids,
PT   useful in preparing a medicament for treating or detecting a
PT   proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT   prostate cancer or tumor.
XX
PS   Claim 12; SEQ ID NO 4238; 7273pp; English.
XX
CC   The invention relates to human tumour-associated antigenic target (TAT)
CC   polypeptides, and their related nucleic acids. The TAT polypeptides are
CC   overexpressed in cancer tissues compared to normal tissues, and may thus
CC   serve as effective targets for the diagnosis and treatment of cancer in
CC   mammals. The invention also relates to nucleic acid and polypeptide
CC   sequences at least 80% identical to the TAT nucleic acids and
CC   polypeptides; expression vectors and host cells comprising a TAT nucleic
CC   acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC   molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC   TAT polypeptide; and methods and compositions for the treatment or
CC   diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC   antibodies, antagonists, binding molecules and compositions are useful
CC   for diagnosing or treating a cell proliferative disorder associated with
CC   increased TAT expression, particularly cancers such as breast cancer,
CC   colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC   cancer, pancreatic cancer, cervical cancer, cancers of the central
CC   nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC   used as hybridisation probes, in chromosome and gene mapping, in
CC   chromosome identification and in gene therapy. The present sequence
CC   represents a TAT polypeptide of the invention
XX
SQ   Sequence 168 AA;

  Query Match           100.0%;  Score 370;  DB 8;  Length 168;
  Best Local Similarity  100.0%;  Pred. No. 1e-37;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
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Db         61 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 120

Qy         61 EKYEKDIAA 69
              |||||||||
Db        121 EKYEKDIAA 129


Search completed: April  6, 2006, 10:19:12
Job time : 83.7533 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 10:19:38 ; Search time 13.1645 Seconds
(without alignments)
504.309 Million cell updates/sec

Title: US-10-717-984-5
Perfect score: 370
Sequence: 1 NAPKRPPSAFFLFCSEYRPK.....QPYEKKAAKLKEKYEKDIAA 69

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	370	100.0	170	2	A27853	nonhistone chromos
2	370	100.0	215	1	NSRTH1	nonhistone chromos
3	370	100.0	215	1	S01947	nonhistone chromos
4	370	100.0	215	2	S02826	nonhistone chromos
5	370	100.0	215	2	I48688	non-histone chromo
6	365	98.6	215	2	A28897	nonhistone chromos
7	360	97.3	216	2	S29857	nonhistone chromos
8	335	90.5	210	2	S62355	high mobility grou
9	324	87.6	186	2	S30221	nonhistone chromos
10	324	87.6	209	1	NSHUH2	nonhistone chromos
11	324	87.6	210	2	A34719	nonhistone chromos
12	321	86.8	207	2	JC1129	nonhistone chromos
13	319	86.2	207	2	JC1114	high-mobility grou
14	316	85.4	210	2	S54774	high mobility grou
15	301	81.4	172	2	A24019	nonhistone chromos
16	301	81.4	204	2	S48708	high-mobility-grou
17	300	81.1	201	2	I50254	HMG-1 - chicken
18	300	81.1	202	2	S22359	nonhistone chromos
19	298	80.5	204	2	T01071	high mobility grou
20	294	79.5	205	2	S26062	nonhistone chromos
21	292	78.9	186	2	B61611	nonhistone chromos
22	263	71.1	215	2	I51067	gene HMG-T2 protei
23	172	46.5	708	2	A41265	DNA-binding protei
24	170	45.9	709	2	A41976	structure-specific
25	168.5	45.5	138	2	T03374	high mobility grou
26	168	45.4	669	2	S78050	high mobility grou
27	166	44.9	200	2	JC4357	HMG1 protein - sea
28	166	44.9	393	2	JC6179	dorsal switch prot
29	166	44.9	393	2	S50068	nonhistone chromos
30	164.5	44.5	141	2	T09581	probable high mobi
31	164	44.3	561	2	S35637	high mobility grou
32	163	44.1	93	2	A35072	nonhistone chromos
33	162.5	43.9	149	2	S39556	high mobility grou
34	160.5	43.4	139	2	T03372	high mobility grou
35	159.5	43.1	141	2	T07377	high mobility grou
36	159	43.0	642	2	T12113	transcription fact
37	158.5	42.8	157	2	B47150	high mobility grou
38	158.5	42.8	161	2	S18991	high mobility grou
39	158.5	42.8	168	2	T03640	high mobility grou
40	157.5	42.6	142	2	T02252	high mobility grou
41	157.5	42.6	144	2	S40302	high mobility grou
42	156.5	42.3	178	2	T51159	HMG protein [impor
43	156	42.2	99	2	S78076	nonhistone chromos
44	155.5	42.0	126	2	T03375	high mobility grou
45	152.5	41.2	141	2	T51598	high mobility grou

ALIGNMENTS

RESULT 1
A27853
nonhistone chromosomal protein HMG-1 - Chinese hamster (fragment)
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: A27853
R;Lee, K.L.D.; Pentecost, B.T.; D'Anna, J.A.; Tobey, R.A.; Gurley, L.R.; Dixon, G.H.
Nucleic Acids Res. 15, 5051-5068, 1987
A;Title: Characterization of cDNA sequences corresponding to three distinct HMG-1 mRNA s
A;Reference number: A27853; MUID:87259986; PMID:3601666
A;Accession: A27853
A;Molecule type: mRNA
A;Residues: 1-170 <LEE>
A;Cross-references: UNIPROT:P07156; UNIPARC:UPI00001771D5
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;1-38/Domain: HMG box homology (fragment) <HMG1>
F;47-121/Domain: HMG box homology <HMG2>

Query Match 100.0%; Score 370; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 3.8e-33;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
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Db         48 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 107

Qy         61 EKYEKDIAA 69
              |||||||||
Db        108 EKYEKDIAA 116
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RESULT 2
NSRTH1
nonhistone chromosomal protein HMG-1 - rat
N;Alternate names: 30K heparin-binding protein, brain; amphoterin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A41175; A27298; A30188; B48771; A48771; C48771
R;Merenmies, J.; Pihlaskari, R.; Laitinen, J.; Wartiovaara, J.; Rauvala, H.
J. Biol. Chem. 266, 16722-16729, 1991
A;Title: 30-kDa heparin-binding protein of brain (amphoterin) involved in neurite outgro
A;Reference number: A41175; MUID:91358468; PMID:1885601
A;Accession: A41175
A;Molecule type: mRNA
A;Residues: 1-215 <MER>
A;Cross-references: UNIPROT:P07155; UNIPARC:UPI00000008A6; GB:M64986; NID:g202884; PIDN:
A;Note: part of this sequence, including the amino end of the mature protein, was confir
A;Note: the authors used antibodies to synthetic peptides to demonstrate this protein in
h-mobility group proteins
R;Paonessa, G.; Frank, R.; Cortese, R.
Nucleic Acids Res. 15, 9077, 1987

A;Title: Nucleotide sequence of rat liver HMG1 cDNA.
A;Reference number: A27298; MUID:88067717; PMID:3684582
A;Accession: A27298
A;Molecule type: mRNA
A;Residues: 1-10,'R',12-82,84-95,97,'AS',100-215 <PAO>
A;Cross-references: UNIPARC:UPI0000173984
R;Rauvala, H.; Merenmies, J.; Pihlaskari, R.; Korkolainen, M.; Huhtala, M.L.; Panula, P.
J. Cell Biol. 107, 2293-2305, 1988
A;Title: The adhesive and neurite-promoting molecule p30: analysis of the amino-terminal
brain neurons.
A;Reference number: A30188; MUID:89066894; PMID:2461949
A;Accession: A30188
A;Molecule type: protein
A;Residues: 2-14,'X',16-21 <RAU>
A;Cross-references: UNIPARC:UPI0000173985
R;Parkkinen, J.; Raulo, E.; Merenmies, J.; Nolo, R.; Kajander, E.O.; Baumann, M.; Rauval
J. Biol. Chem. 268, 19726-19738, 1993
A;Title: Amphoterin, the 30-kDa protein in a family of HMG1-type polypeptides. Enhanced
A;Reference number: A48771; MUID:93374971; PMID:8366113
A;Accession: B48771
A;Status: preliminary
A;Molecule type: protein
A;Residues: 98-105,'X',107-112 <PA2>
A;Cross-references: UNIPARC:UPI0000173986
A;Experimental source: postnatal brain
A;Note: sequence extracted from NCBI backbone (NCBIP:137788)
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;2-215/Product: nonhistone chromosomal protein HMG-1 #status experimental <MAT>
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

Query Match 100.0%; Score 370; DB 1; Length 215;
Best Local Similarity 100.0%; Pred. No. 4.9e-33;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 93 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 152

Qy 61 EKYEKDIAA 69
|||||||||
Db 153 EKYEKDIAA 161

RESULT 3
S01947
nonhistone chromosomal protein HMG-1 - bovine
N;Alternate names: 33K protein; high-mobility-group protein HMG-1
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1989 #sequence_revision 22-Apr-1995 #text_change 09-Jul-2004
C;Accession: S01947; A61611; S10959; I45910
R;Kaplan, D.J.; Duncan, C.H.
Nucleic Acids Res. 16, 10375, 1988
A;Title: Full length cDNA sequence for bovine high mobility group 1 (HMG1) protein.
A;Reference number: S01947; MUID:89057489; PMID:3194213
A;Accession: S01947
A;Molecule type: mRNA
A;Residues: 1-215 <KAP>
A;Cross-references: UNIPROT:P10103; UNIPARC:UPI000016C31D; EMBL:X12796; NID:g416; PIDN:C
R;Walker, J.M.; Gooderham, K.; Hastings, J.R.B.; Mayes, E.; Johns, E.W.
FEBS Lett. 122, 264-270, 1980
A;Title: The primary structures of non-histone chromosomal proteins HMG 1 and 2.
A;Reference number: A61611; MUID:81138848; PMID:7202717
A;Accession: A61611
A;Molecule type: protein
A;Residues: 2-22,'S',24-40;48-105,'A',107-157,'X',160-193,'D',195 <WAL>
A;Cross-references: UNIPARC:UPI0000173987; UNIPARC:UPI0000173988
R;Christen, T.; Bischoff, M.; Hobi, R.; Kuenzle, C.C.
FEBS Lett. 267, 139-141, 1990
A;Title: High mobility group proteins 1 and 2 bind preferentially to brominated poly(dG-
A;Reference number: S10726; MUID:90306387; PMID:2365081
A;Accession: S10959
A;Molecule type: protein
A;Residues: 2-22,'X',24-38 <CHR>
A;Cross-references: UNIPARC:UPI0000173989
R;Pentecost, B.T.; Dixon, G.H.
Biosci. Rep. 4, 49-57, 1984
A;Title: Isolation and partial sequence of bovine cDNA clones for the high-mobility-group
A;Reference number: I45910; MUID:84128872; PMID:6141822
A;Accession: I45910
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 'PGG',119,'V',121-215 <PEN>
A;Cross-references: UNIPARC:UPI000016C31E; GB:M26110; NID:g163156; PIDN:AAA30567.1; PID:g
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; duplication; nucleus
F;2-215/Product: nonhistone chromosomal protein HMG-1 #status predicted <MAT>
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

Query Match 100.0%; Score 370; DB 1; Length 215;
Best Local Similarity 100.0%; Pred. No. 4.9e-33;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
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Db 93 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 152

Qy 61 EKYEKDIAA 69
|||||||||
Db 153 EKYEKDIAA 161

RESULT 4
S02826
nonhistone chromosomal protein HMG-1 - human
C;Species: Homo sapiens (man)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C;Accession: S02826; A33178; G33178
R;Wen, L.; Huang, J.K.; Johnson, B.H.; Reeck, G.R.
Nucleic Acids Res. 17, 1197-1214, 1989
A;Title: A human placental cDNA clone that encodes nonhistone chromosomal protein HMG-1.
A;Reference number: S02826; MUID:89160247; PMID:2922262
A;Accession: S02826
A;Molecule type: mRNA
A;Residues: 1-215 <WEN>
A;Cross-references: UNIPROT:P09429; UNIPARC:UPI00000015ED; EMBL:X12597; NID:g32326; PIDN
R;Ward, L.D.; Hong, J.; Whitehead, R.H.; Simpson, R.J.
Electrophoresis 11, 883-891, 1990
A;Title: Development of a database of amino acid sequences for human colon carcinoma prot
A;Reference number: A33178; MUID:91176935; PMID:2079031
A;Accession: A33178
A;Molecule type: protein
A;Residues: 2-13,'XXF' <WAR>
A;Cross-references: UNIPARC:UPI00001771D7
A;Accession: G33178
A;Molecule type: protein
A;Residues: 2-13,'XX',16-22 <WA2>
A;Cross-references: UNIPARC:UPI00001771D7
C;Genetics:
A;Gene: GDB:HMG1
A;Cross-references: GDB:133789; OMIM:163905
A;Map position: 13q12-13q12
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

Query Match 100.0%; Score 370; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 4.9e-33;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 93 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 152

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Qy          61 EKYEKDIAA 69
               |||||||||
Db         153 EKYEKDIAA 161


RESULT 5
I48688
non-histone chromosomal high-mobility group 1 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48688; A55402; I57021
R;Yotov, W.V.; St-Arnaud, R.
Nucleic Acids Res. 20, 3516, 1992
A;Title: Nucleotide sequence of a mouse cDNA encoding the nonhistone chromosomal high mo
A;Reference number: I48687; MUID:92335012; PMID:1630928
A;Accession: I48688
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-215 <RES>
A;Cross-references: UNIPROT:P07155; UNIPARC:UPI00000008A6; EMBL:Z11997; NID:g53381; PIDN
R;Ferrari, S.; Ronfani, L.; Calogero, S.; Bianchi, M.E.
J. Biol. Chem. 269, 28803-28808, 1994
A;Title: The mouse gene coding for high mobility group 1 protein (HMG1).
A;Reference number: A55402; MUID:95050689; PMID:7961836
A;Accession: A55402
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-189,'E',191-215 <FER>
A;Cross-references: UNIPARC:UPI000016CDD6; EMBL:X80457; NID:g620097; PIDN:CAA56631.1; PI
R;Pauken, C.M.; Nagle, D.L.; Bucan, M.; Lo, C.W.
Mamm. Genome 5, 91-99, 1994
A;Title: Molecular cloning, expression analysis, and chromosomal localization of mouse H
A;Reference number: I57021; MUID:94235965; PMID:8180479
A;Accession: I57021
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-215 <RE2>
A;Cross-references: UNIPARC:UPI00000008A6; EMBL:U00431; NID:g437101; PIDN:AAA20508.1; PI
C;Genetics:
A;Gene: hmg1
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

  Query Match             100.0%;  Score 370;  DB 2;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-33;
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Qy          61 EKYEKDIAA 69
               |||||||||
Db         153 EKYEKDIAA 161


RESULT 6
A28897
nonhistone chromosomal protein HMG-1 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: A28897
R;Tsuda, K.; Kikuchi, M.; Mori, K.; Waga, S.; Yoshida, M.
Biochemistry 27, 6159-6163, 1988
A;Title: Primary structure of non-histone protein HMG1 revealed by the nucleotide sequen
A;Reference number: A28897; MUID:89050965; PMID:3191113
A;Accession: A28897
A;Molecule type: mRNA
A;Residues: 1-215 <TSU>
A;Cross-references: UNIPROT:P12682; UNIPARC:UPI000016C6C4; GB:M21683; GB:M21684; NID:g16
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

  Query Match             98.6%;  Score 365;  DB 2;  Length 215;
  Best Local Similarity   98.6%;  Pred. No. 1.7e-32;
  Matches   68;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
               |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db          93 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKHPYEKKAAKLK 152

Qy          61 EKYEKDIAA 69
               |||||||||
Db         153 EKYEKDIAA 161


RESULT 7
S29857
nonhistone chromosomal protein HMG-1 - human
C;Species: Homo sapiens (man)
C;Date: 08-Dec-1993 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C;Accession: S29857
R;Stros, M.; Dixon, G.H.
Biochim. Biophys. Acta 1172, 231-235, 1993
A;Title: A retropseudogene for non-histone chromosomal protein HMG-1.
A;Reference number: S29857; MUID:93176821; PMID:8439568
A;Accession: S29857
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-216 <STR>
A;Cross-references: UNIPARC:UPI000011DFAA; EMBL:L08048; NID:g184250; PIDN:AAA64970.1; PI
A;Note: the authors did not translate the codon for residue 1
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

  Query Match             97.3%;  Score 360;  DB 2;  Length 216;
  Best Local Similarity   98.6%;  Pred. No. 6.1e-32;
  Matches   68;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
               ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          93 NAPKRLPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 152

Qy          61 EKYEKDIAA 69
               |||||||||
Db         153 EKYEKDIAA 161


RESULT 8
S62355
high mobility group protein 1 - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S62355
R;Nightingale, K.; Dimitrov, S.; Reeves, R.; Wolffe, A.P.
EMBO J. 15, 548-561, 1996
A;Title: Evidence for a shared structural role for HMG1 and linker histones B4 and H1 in
A;Reference number: S62355; MUID:96174815; PMID:8599938
A;Accession: S62355
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-210 <NIG>
A;Cross-references: UNIPROT:Q91596; UNIPARC:UPI00000FB3E3; EMBL:U21933; NID:g709958; PID
A;Note: the authors did not translate the codon for residue 1
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
F;6-82/Domain: HMG box homology <HMG1>
F;91-165/Domain: HMG box homology <HMG2>

  Query Match             90.5%;  Score 335;  DB 2;  Length 210;
```

```
  Best Local Similarity   85.5%;  Pred. No. 3.2e-29;
  Matches   59;  Conservative    7;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              |||||||||||||||::|||||||||| :|||:||||||||||| ||| |||::|||||
Db         92 NAPKRPPSAFFLFCSDFRPKIKGEHPGSTIGDIAKKLGEMWNNTATDDKLPYERRAAKLK 151

Qy         61 EKYEKDIAA 69
              |||||||:||
Db        152 EKYEKDVAA 160


RESULT 9
S30221
nonhistone chromosomal protein HMG-2B - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: S30221
R;Alexandre, S.; Li, W.W.; Lee, A.S.
Nucleic Acids Res. 20, 6413, 1992
A;Title: A human HMG2 cDNA with a novel 3'-untranslated region.
A;Reference number: S30221; MUID:93117123; PMID:1475204
A;Accession: S30221
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-186 <ALE>
A;Cross-references: UNIPROT:P26583; UNIPARC:UPI000016AA6C; EMBL:Z17240; NID:g32334; PIDN
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1992
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein
F;1-60/Domain: HMG box homology (fragment) <HMG>
F;69-143/Domain: HMG box homology <HMG1>

  Query Match             87.6%;  Score 324;  DB 2;  Length 186;
  Best Local Similarity   87.0%;  Pred. No. 4.4e-28;
  Matches   60;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              |||||||||||||||:|||||  |||||||||  ||||||||:  :| ||||||:||||||
Db         70 NAPKRPPSAFFLFCSEHRPKIKSEHPGLSIGDTAKKLGEMWSEQSAKDKQPYEQKAAKLK 129

Qy         61 EKYEKDIAA 69
              |||||||||
Db        130 EKYEKDIAA 138


RESULT 10
NSHUH2
nonhistone chromosomal protein HMG-2 - human
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: A42425; S20061; S18068
R;Shirakawa, H.; Yoshida, M.
J. Biol. Chem. 267, 6641-6645, 1992
A;Title: Structure of a gene coding for human HMG2 protein.
A;Reference number: A42425; MUID:92202209; PMID:1551873
A;Accession: A42425
A;Molecule type: DNA
A;Residues: 2-209 <SHI>
A;Cross-references: UNIPROT:P26583; UNIPARC:UPI000012CA25; GB:M83665; NID:g184235; PIDN:
A;Note: sequence extracted from NCBI backbone (NCBIN:89899, NCBIP:89900)
A;Note: initiator Met not shown
R;Majumdar, A.; Brown, D.; Kerby, S.; Rudzinski, I.; Polte, T.; Randhawa, Z.; Seidman, M
Nucleic Acids Res. 19, 6643, 1991
A;Title: Sequence of human HMG2 cDNA.
A;Reference number: S20061; MUID:92093633; PMID:1754403
A;Accession: S20061
A;Molecule type: mRNA
A;Residues: 1-209 <MAJ>
A;Cross-references: UNIPARC:UPI000013E34D; EMBL:X62534; NID:g32332; PIDN:CAA44395.1; PID
C;Genetics:
A;Gene: GDB:NHCP2
A;Cross-references: GDB:119451; OMIM:118880
A;Map position: 7pter-7qter
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

  Query Match             87.6%;  Score 324;  DB 1;  Length 209;
  Best Local Similarity   87.0%;  Pred. No. 5e-28;
  Matches   60;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              |||||||||||||||:|||||  |||||||||  ||||||||:  :| ||||||:||||||
Db         93 NAPKRPPSAFFLFCSEHRPKIKSEHPGLSIGDTAKKLGEMWSEQSAKDKQPYEQKAAKLK 152

Qy         61 EKYEKDIAA 69
              |||||||||
Db        153 EKYEKDIAA 161


RESULT 11
A34719
nonhistone chromosomal protein HMG-2 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 09-Jul-2004
C;Accession: A34719
R;Shirakawa, H.; Tsuda, K.; Yoshida, M.
Biochemistry 29, 4419-4423, 1990
A;Title: Primary structure of non-histone chromosomal protein HMG2 revealed by the nucle
A;Reference number: A34719; MUID:90275208; PMID:2350545
A;Accession: A34719
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-210 <SHI>
A;Cross-references: UNIPROT:P17741; UNIPARC:UPI000016C6C5; GB:J02895; NID:g164491; PIDN:
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

  Query Match             87.6%;  Score 324;  DB 2;  Length 210;
  Best Local Similarity   87.0%;  Pred. No. 5.1e-28;
  Matches   60;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              |||||||||||||||:|||||  |||||||||  ||||||||:  :| ||||||:||||||
Db         93 NAPKRPPSAFFLFCSEHRPKIKSEHPGLSIGDTAKKLGEMWSEQSAKDKQPYEQKAAKLK 152

Qy         61 EKYEKDIAA 69
              |||||||||
Db        153 EKYEKDIAA 161


RESULT 12
JC1129
nonhistone chromosomal protein HMG-2 - chicken
N;Alternate names: high-mobility-group protein 2
C;Species: Gallus gallus (chicken)
C;Date: 05-Mar-1993 #sequence_revision 05-Mar-1993 #text_change 09-Jul-2004
C;Accession: JC1129
R;Sparrow, D.B.; Wells, J.R.E.
Gene 114, 289-290, 1992
A;Title: Sequence of a cDNA encoding chicken high-mobility-group protein-2.
A;Reference number: JC1129; MUID:92290291; PMID:1601311
A;Accession: JC1129
A;Molecule type: mRNA
A;Residues: 1-207 <SPA>
A;Cross-references: UNIPROT:P26584; UNIPARC:UPI0000171348; GB:M80574; NID:g211928; PIDN:
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

  Query Match             86.8%;  Score 321;  DB 2;  Length 207;
```

```
  Best Local Similarity   85.5%;  Pred. No. 1.1e-27;
  Matches   59;  Conservative    5;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||||||||||||:|||||  :||||||||  ||||||||:  :|  ||||||:||||||
Db         93 NAPKRPPSAFFLFCSEHRPKIKNDHPGLSIGDTAKKLGEMWSEQSAKDKQPYEQKAAKLK 152

Qy         61 EKYEKDIAA 69
              |||||||||
Db        153 EKYEKDIAA 161


RESULT 13
JC1114
high-mobility group protein 2 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004
C;Accession: JC1114
R;Davis, D.L.; Burch, J.B.E.
Gene 113, 251-256, 1992
A;Title: Isolation of a chicken HMG2 cDNA clone and evidence for an HMG2-specific 3'-unt
A;Reference number: JC1114; MUID:92241676; PMID:1572546
A;Accession: JC1114
A;Molecule type: mRNA
A;Residues: 1-207 <DAV>
A;Cross-references: UNIPROT:P26584; UNIPARC:UPI0000171347; GB:M83235; NID:g211926; PIDN:
C;Comment: The high mobility group proteins are among the most abundant nonhistone chrom
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

  Query Match             86.2%;  Score 319;  DB 2;  Length 207;
  Best Local Similarity   85.5%;  Pred. No. 1.8e-27;
  Matches   59;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||||||||||||:|||||  :||||||||  ||||||||:   | ||||||:||||||
Db         93 NAPKRPPSAFFLFCSEHRPKIKNDHPGLSIGDTAKKLGEMWSEQLAKDKQPYEQKAAKLK 152

Qy         61 EKYEKDIAA 69
              |||||||||
Db        153 EKYEKDIAA 161


RESULT 14
S54774
high mobility group 2 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S54774; S52211
R;Zwilling, S.; Koenig, H.; Wirth, T.
EMBO J. 14, 1198-1208, 1995
A;Title: High mobility group protein 2 functionally interacts with the POU domains of oc
A;Reference number: S54774; MUID:95237201; PMID:7720710
A;Accession: S54774
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-210 <ZWI>
A;Cross-references: UNIPROT:P30681; UNIPARC:UPI000016432C; EMBL:Z46757; NID:g609168; PID
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

  Query Match             85.4%;  Score 316;  DB 2;  Length 210;
  Best Local Similarity   87.0%;  Pred. No. 3.8e-27;
  Matches   60;  Conservative    3;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||||||||||||| ||||| |||||||||  ||||||||:  :|  ||||||:||||||
Db         93 NAPKRPPSAFFLFCSENRPKIKIEHPGLSIGDTAKKLGEMWSEQSAKDKQPYEQKAAKLK 152

Qy         61 EKYEKDIAA 69
              |||||||||
Db        153 EKYEKDIAA 161


RESULT 15
A24019
nonhistone chromosomal protein HMG-T - trout (fragment)
N;Alternate names: HMG-T
C;Species: Salmo sp. (trout)
C;Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 09-Jul-2004
C;Accession: A24019
R;Pentecost, B.T.; Wright, J.M.; Dixon, G.H.
Nucleic Acids Res. 13, 4871-4888, 1985
A;Title: Isolation and sequence of cDNA clones coding for a member of the family of high
A;Reference number: A24019; MUID:85269614; PMID:4022777
A;Accession: A24019
A;Molecule type: mRNA
A;Residues: 1-172 <PEN>
A;Cross-references: UNIPROT:P07746; UNIPARC:UPI00001771D6
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;1-50/Domain: HMG box homology (fragment) <HMG1>
F;59-133/Domain: HMG box homology <HMG2>

  Query Match             81.4%;  Score 301;  DB 2;  Length 172;
  Best Local Similarity   78.3%;  Pred. No. 1.3e-25;
  Matches   54;  Conservative    8;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              |||||| |||||:||:::||::||| |||||||||||||| |||  |:|| ||||||:|||
Db         60 NAPKRPPSSAFFIFCADFRPQVKGETPGLSIGDVAKKLGEKWNNLTAEDKVPYEKKASKLK 119

Qy         61 EKYEKDIAA 69
              ||||||| |
Db        120 EKYEKDITA 128


Search completed: April  6, 2006, 10:26:19
Job time : 14.1645 secs
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OM protein - protein search, using sw model

Run on: April 6, 2006, 10:13:48 ; Search time 81.4836 Seconds
(without alignments)
597.439 Million cell updates/sec

Title: US-10-717-984-5
Perfect score: 370
Sequence: 1 NAPKRPPSAFFLFCSEYRPK.....QPYEKKAAKLKEKYEKDIAA 69

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	370	100.0	178	2	Q8C7C4_MOUSE	Q8c7c4 mus musculu
2	370	100.0	180	1	HMG1_CRIGR	P07156 cricetulus
3	370	100.0	181	2	Q8BNM0_MOUSE	Q8bnm0 mus musculu
4	370	100.0	192	2	Q5T7C5_HUMAN	Q5t7c5 homo sapien
5	370	100.0	214	1	HMG1_BOVIN	P10103 bos taurus
6	370	100.0	214	1	HMG1_CANFA	Q6yka4 canis famil
7	370	100.0	214	1	HMG1_HUMAN	P09429 homo sapien
8	370	100.0	214	1	HMG1_MOUSE	P63158 mus musculu
9	370	100.0	214	1	HMG1_RAT	P63159 rattus norv
10	370	100.0	215	2	Q5T7C3_HUMAN	Q5t7c3 homo sapien
11	370	100.0	215	2	Q4R844_MACFA	Q4r844 macaca fasc
12	370	100.0	215	2	O88611_SPAEH	O88611 spalax leuc
13	370	100.0	215	2	O88612_SPAEH	O88612 spalax leuc
14	370	100.0	215	2	Q9QWY6_SPAEH	Q9qwy6 spalax leuc
15	370	100.0	215	2	Q9QX40_SPAEH	Q9qx40 spalax leuc
16	370	100.0	215	2	Q548R9_RAT	Q548r9 rattus norv
17	370	100.0	215	2	Q58EV5_MOUSE	Q58ev5 m high mobi
18	366	98.9	214	2	Q9PUK9_CHICK	Q9puk9 gallus gall
19	366	98.9	215	2	Q9YH06_CHICK	Q9yh06 gallus gall
20	365	98.6	214	1	HMG1_PIG	P12682 sus scrofa
21	365	98.6	215	2	Q14321_HUMAN	Q14321 homo sapien
22	364	98.4	215	2	Q6P202_MOUSE	Q6p202 mus musculu
23	360	97.3	215	2	Q8BQ02_MOUSE	Q8bq02 mus musculu
24	359	97.0	206	2	Q5BKQ1_MOUSE	Q5bkq1 mus musculu
25	356	96.2	211	1	HMG1X_HUMAN	Q9ugv6 homo sapien
26	355	95.9	211	2	Q9NQJ4_HUMAN	Q9nqj4 homo sapien
27	352	95.1	157	2	Q5T7C2_HUMAN	Q5t7c2 homo sapien
28	352	95.1	158	2	Q5T7C4_HUMAN	Q5t7c4 homo sapien
29	352	95.1	176	2	Q59GW1_HUMAN	Q59gw1 homo sapien
30	341	92.2	211	2	Q6P4N5_XENTR	Q6p4n5 xenopus tro
31	337	91.1	211	2	Q7SZ42_XENLA	Q7sz42 xenopus lae
32	335	90.5	210	2	Q91596_XENLA	Q91596 xenopus lae
33	335	90.5	210	2	Q6GNQ5_XENLA	Q6gnq5 xenopus lae
34	324	87.6	195	2	Q96J53_HUMAN	Q96j53 homo sapien
35	324	87.6	208	1	HMG2_HUMAN	P26583 homo sapien
36	324	87.6	208	2	Q5U071_HUMAN	Q5u071 homo sapien
37	324	87.6	209	1	HMG2_PIG	P17741 sus scrofa
38	324	87.6	209	1	HMG2_RAT	P52925 rattus norv
39	324	87.6	209	2	Q5U072_HUMAN	Q5u072 homo sapien
40	324	87.6	210	2	Q5FVP0_RAT	Q5fvp0 rattus norv
41	324	87.6	242	1	SP100_HYLLA	Q9n1q5 hylobates l
42	323.5	87.4	199	2	Q8CH24_MOUSE	Q8ch24 mus musculu
43	319	86.2	200	2	Q6Y235_PAGMA	Q6y235 pagrus majo
44	319	86.2	206	1	HMG2_CHICK	P26584 gallus gall
45	319	86.2	215	1	SP100_PANTR	Q9n1q7 pan troglod

ALIGNMENTS

RESULT 1
Q8C7C4_MOUSE
ID Q8C7C4_MOUSE PRELIMINARY; PRT; 178 AA.
AC Q8C7C4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-
DE length enriched library, clone:C920030E14 product:high mobility group
DE box 1, full insert sequence. (Fragment).
GN Name=Hmgb1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";

```
RL   Nature 420:563-573(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK050659; BAC34367.1; -; mRNA.
DR   HSSP; P07156; 1NHN.
DR   SMR; Q8C7C4; 2-84, 93-171.
DR   MGI; MGI:96113; Hmgb1.
DR   GO; GO:0005615; C:extracellular space; IDA.
DR   GO; GO:0005634; C:nucleus; TAS.
DR   GO; GO:0030235; F:nitric-oxide synthase regulator activity; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0006809; P:nitric oxide biosynthesis; IDA.
DR   GO; GO:0006810; P:transport; IDA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
FT   NON_TER     178    178
SQ   SEQUENCE   178 AA;  20303 MW;  155FD80D52960A62 CRC64;

  Query Match             100.0%;  Score 370;  DB 2;  Length 178;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-31;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 152

Qy         61 EKYEKDIAA 69
              |||||||||
Db        153 EKYEKDIAA 161

RESULT 2
```

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HMG1_CRIGR
ID   HMG1_CRIGR     STANDARD;      PRT;   180 AA.
AC   P07156;
DT   01-APR-1988 (Rel. 07, Created)
DT   01-APR-1988 (Rel. 07, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   High mobility group protein 1 (HMG-1) (High mobility group protein B1)
DE   (Fragment).
GN   Name=HMGB1; Synonyms=HMG-1, HMG1;
OS   Cricetulus griseus (Chinese hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Cricetidae; Cricetinae; Cricetulus.
OX   NCBI_TaxID=10029;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX   MEDLINE=87259986; PubMed=3601666;
RA   Lee K.-L.D., Pentecost B.T., D'Anna J.A., Tobey R.A., Gurley L.R.,
RA   Dixon G.H.;
RT   "Characterization of cDNA sequences corresponding to three distinct
RT   HMG-1 mRNA species in line CHO Chinese hamster cells and cell cycle
RT   expression of the HMG-1 gene.";
RL   Nucleic Acids Res. 15:5051-5068(1987).
RN   [2]
RP   STRUCTURE BY NMR OF 57-136.
RX   MEDLINE=93347974; PubMed=8346022;
RA   Read C.M., Cary P.D., Crane-Robinson C., Driscoll P.C., Norman D.G.;
RT   "Solution structure of a DNA-binding domain from HMG1.";
RL   Nucleic Acids Res. 21:3427-3436(1993).
CC   -!- FUNCTION: Binds preferentially single-stranded DNA and unwinds
CC       double stranded DNA.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
CC   -!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; Y00365; CAA68441.1; -; Genomic_DNA.
DR   PIR; A27853; A27853.
DR   PDB; 1HSM; NMR; @=58-136.
DR   PDB; 1HSN; NMR; @=58-136.
DR   PDB; 1NHM; NMR; @=58-136.
DR   PDB; 1NHN; NMR; @=58-136.
DR   SMR; P07156; 1-49.
DR   GO; GO:0000793; C:condensed chromosome; ISS.
DR   GO; GO:0008301; F:DNA bending activity; ISS.
DR   GO; GO:0005515; F:protein binding; ISS.
DR   GO; GO:0006288; P:base-excision repair, DNA ligation; ISS.
DR   GO; GO:0006310; P:DNA recombination; ISS.
DR   GO; GO:0006281; P:DNA repair; ISS.
DR   GO; GO:0006268; P:DNA unwinding; ISS.
DR   GO; GO:0006325; P:establishment and/or maintenance of chromat. . .; ISS.
DR   GO; GO:0017055; P:negative regulation of transcriptional prei. . .; ISS.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
KW   3D-structure; Chromosomal protein; DNA-binding; Nuclear protein;
KW   Repeat.
FT   DNA_BIND     <1     44       HMG box 1.
FT   DNA_BIND     60     128      HMG box 2.
FT   COMPBIAS     151    180      Asp/Glu-rich (acidic).
FT   NON_TER       1      1
FT   HELIX        67     81
FT   TURN         83     84
FT   TURN         87     88
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FT   HELIX        89     97
FT   TURN         98    100
FT   HELIX       103    128
SQ   SEQUENCE   180 AA;  20904 MW;  F624392F41609854 CRC64;

  Query Match             100.0%;  Score 370;  DB 1;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-31;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         58 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 117

Qy         61 EKYEKDIAA 69
              |||||||||
Db        118 EKYEKDIAA 126


RESULT 3
Q8BNM0_MOUSE
ID   Q8BNM0_MOUSE PRELIMINARY;      PRT;   181 AA.
AC   Q8BNM0;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mus musculus 7 days embryo whole body cDNA, RIKEN full-length enriched
DE   library, clone:C430013M12 product:high mobility group box 1, full
DE   insert sequence. (Fragment).
GN   Name=Hmgb1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK082902; BAC38678.1; -; mRNA.
DR   HSSP; P07156; 1NHN.
DR   SMR; Q8BNM0; 2-84, 93-171.
DR   MGI; MGI:96113; Hmgb1.
DR   GO; GO:0005615; C:extracellular space; IDA.
DR   GO; GO:0005634; C:nucleus; TAS.
DR   GO; GO:0030235; F:nitric-oxide synthase regulator activity; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0006809; P:nitric oxide biosynthesis; IDA.
DR   GO; GO:0006810; P:transport; IDA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
FT   NON_TER     181    181
SQ   SEQUENCE   181 AA;  20648 MW;  B31D82055FD80D52 CRC64;

  Query Match             100.0%;  Score 370;  DB 2;  Length 181;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-31;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 152

Qy         61 EKYEKDIAA 69
              |||||||||
Db        153 EKYEKDIAA 161


RESULT 4
Q5T7C5_HUMAN
```

```
ID   Q5T7C5_HUMAN PRELIMINARY;      PRT;   192 AA.
AC   Q5T7C5;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   High-mobility group box 1 (Fragment).
GN   Name=HMGB1; ORFNames=RP11-550P23.1-001;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Pelan S.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL353648; CAI15602.1; -; Genomic_DNA.
DR   SMR; Q5T7C5; 2-84, 93-171.
DR   GO; GO:0000785; C:chromatin; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
FT   NON_TER     192    192
SQ   SEQUENCE   192 AA;  22050 MW;  6A52DB61DA307C1D CRC64;

  Query Match             100.0%;  Score 370;  DB 2;  Length 192;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-31;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 152

Qy         61 EKYEKDIAA 69
              |||||||||
Db        153 EKYEKDIAA 161


RESULT 5
HMG1_BOVIN
ID   HMG1_BOVIN     STANDARD;      PRT;   214 AA.
AC   P10103;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-AUG-1990 (Rel. 15, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   High mobility group protein 1 (HMG-1) (High mobility group protein
DE   B1).
GN   Name=HMGB1; Synonyms=HMG1;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   STRAIN=Holstein; TISSUE=Fetal thymus;
RX   MEDLINE=89057489; PubMed=3194213;
RA   Kaplan D.J., Duncan C.H.;
RT   "Full length cDNA sequence for bovine high mobility group 1 (HMG1)
RT   protein.";
RL   Nucleic Acids Res. 16:10375-10375(1988).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 115-214.
RX   MEDLINE=84128872; PubMed=6141822;
RA   Pentecost B., Dixon G.H.;
RT   "Isolation and partial sequence of bovine cDNA clones for the high-
RT   mobility-group protein (HMG-1).";
RL   Biosci. Rep. 4:49-57(1984).
RN   [3]
RP   PROTEIN SEQUENCE OF 1-37; 45-156 AND 158-194.
RX   MEDLINE=81138848; PubMed=7202717; DOI=10.1016/0014-5793(80)80453-4;
RA   Walker J.M., Gooderham K., Hastings J.R., Mayes E., Johns E.W.;
RT   "The primary structures of non-histone chromosomal proteins HMG 1 and
RT   2.";
RL   FEBS Lett. 122:264-270(1980).
RN   [4]
RP   PROTEIN SEQUENCE OF 1-36.
RX   MEDLINE=90306387; PubMed=2365081; DOI=10.1016/0014-5793(90)80308-6;
RA   Christen T., Bischoff M., Hobi R., Kuenzle C.C.;
RT   "High mobility group proteins 1 and 2 bind preferentially to
RT   brominated poly(dG-dC).poly(dG-dC) in the Z-DNA conformation but not
RT   to other types of Z-DNA.";
RL   FEBS Lett. 267:139-141(1990).
CC   -!- FUNCTION: Binds preferentially single-stranded DNA and unwinds
CC       double stranded DNA.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
CC   -!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; X12796; CAA31284.1; -; mRNA.
DR   EMBL; M26110; AAA30567.1; -; mRNA.
DR   PIR; S01947; S01947.
DR   HSSP; P07156; 1NHN.
DR   SMR; P10103; 1-83, 92-170.
DR   GO; GO:0000793; C:condensed chromosome; ISS.
DR   GO; GO:0008301; F:DNA bending activity; ISS.
DR   GO; GO:0005515; F:protein binding; ISS.
DR   GO; GO:0006288; P:base-excision repair, DNA ligation; ISS.
DR   GO; GO:0006310; P:DNA recombination; ISS.
DR   GO; GO:0006281; P:DNA repair; ISS.
DR   GO; GO:0006268; P:DNA unwinding; ISS.
DR   GO; GO:0006325; P:establishment and/or maintenance of chromat. . .; ISS.
DR   GO; GO:0017055; P:negative regulation of transcriptional prei. . .; ISS.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
KW   Chromosomal protein; Direct protein sequencing; DNA-binding;
KW   Nuclear protein; Repeat.
FT   INIT_MET      0      0
FT   DNA_BIND      8     78       HMG box 1.
FT   DNA_BIND     94    162       HMG box 2.
FT   COMPBIAS    185    214       Asp/Glu-rich (acidic).
FT   CONFLICT     22     22       C -> S (in Ref. 3).
FT   CONFLICT    105    105       C -> A (in Ref. 3).
FT   CONFLICT    115    119       EHPGL -> PGGGV (in Ref. 2).
FT   CONFLICT    193    193       E -> D (in Ref. 3).
SQ   SEQUENCE   214 AA;  24777 MW;  B283A80FC7F0F433 CRC64;

  Query Match             100.0%;  Score 370;  DB 1;  Length 214;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-31;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 151

Qy         61 EKYEKDIAA 69
              |||||||||
Db        152 EKYEKDIAA 160
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RESULT 6
HMG1_CANFA
ID   HMG1_CANFA     STANDARD;      PRT;   214 AA.
AC   Q6YKA4;
DT   10-MAY-2005 (Rel. 47, Created)
DT   10-MAY-2005 (Rel. 47, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   High mobility group protein 1 (HMG-1) (High mobility group protein
DE   B1).
GN   Name=HMGB1;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC   Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA].
RX   MEDLINE=22932580; PubMed=14571134; DOI=10.1159/000073415;
RA   Murua Escobar H., Meyer B., Richter A., Becker K., Flohr A.M.,
RA   Bullerdiek J., Nolte I.;
RT   "Molecular characterization of the canine HMGB1.";
RL   Cytogenet. Genome Res. 101:33-38(2003).
CC   -!- FUNCTION: Binds preferentially single-stranded DNA and unwinds
CC       double stranded DNA (By similarity).
CC   -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC   -!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
CC   -!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AY135519; AAN11296.1; -; mRNA.
DR   EMBL; AY135521; AAN11319.1; -; Genomic_DNA.
DR   HSSP; P07155; 1AAB.
DR   SMR; Q6YKA4; 1-83, 92-170.
DR   Ensembl; ENSCAFG00000006597; Canis familiaris.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
KW   Chromosomal protein; DNA-binding; Nuclear protein; Repeat.
FT   INIT_MET      0      0       By similarity.
FT   DNA_BIND      8     78       HMG box 1.
FT   DNA_BIND     94    162       HMG box 2.
FT   COMPBIAS    185    214       Asp/Glu-rich (acidic).
SQ   SEQUENCE   214 AA;  24763 MW;  B3C6A80FC7F0F433 CRC64;

  Query Match             100.0%;  Score 370;  DB 1;  Length 214;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-31;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 151

Qy         61 EKYEKDIAA 69
              |||||||||
Db        152 EKYEKDIAA 160


RESULT 7
HMG1_HUMAN
ID   HMG1_HUMAN     STANDARD;      PRT;   214 AA.
AC   P09429; Q6IBE1;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-AUG-1990 (Rel. 15, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   High mobility group protein 1 (HMG-1) (High mobility group protein
DE   B1).
GN   Name=HMGB1; Synonyms=HMG1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=89160247; PubMed=2922262;
RA   Wen L., Huang J.K., Johnson B.H., Reeck G.R.;
RT   "A human placental cDNA clone that encodes nonhistone chromosomal
RT   protein HMG-1.";
RL   Nucleic Acids Res. 17:1197-1214(1989).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX   MEDLINE=96299787; PubMed=8661151; DOI=10.1006/geno.1996.0369;
RA   Ferrari S., Finelli P., Rocchi M., Bianchi M.E.;
RT   "The active gene that encodes human high mobility group 1 protein
RT   (HMG1) contains introns and maps to chromosome 13.";
RL   Genomics 35:367-371(1996).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RA   He F.T., Yang Z.H., Ji Q., Li R., Peng J., Jiang Y., Zhong X.;
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Small intestine;
RG   The German cDNA consortium;
RL   Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA   Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RT   "Cloning of human full open reading frames in Gateway(TM) system entry
RT   vector (pDONR201).";
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA   Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA   Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA   Phelan M., Farmer A.;
RT   "Cloning of human full-length CDSs in BD Creator(TM) system donor
RT   vector.";
RL   Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Brain, Cervix, and Testis;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [8]
RP   PROTEIN SEQUENCE OF 57-64 AND 112-126.
```

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RC   TISSUE=Mammary carcinoma;
RX   MEDLINE=97295304; PubMed=9150946;
RA   Rasmussen R.K., Ji H., Eddes J.S., Moritz R.L., Reid G.E.,
RA   Simpson R.J., Dorow D.S.;
RT   "Two-dimensional electrophoretic analysis of human breast carcinoma
RT   proteins: mapping of proteins that bind to the SH3 domain of mixed
RT   lineage kinase MLK2.";
RL   Electrophoresis 18:588-598(1997).
CC   -!- FUNCTION: Binds preferentially single-stranded DNA and unwinds
CC       double stranded DNA.
CC   -!- INTERACTION:
CC       P04637:TP53; NbExp=1; IntAct=EBI-389432, EBI-366083;
CC       O15350:TP73; NbExp=1; IntAct=EBI-389432, EBI-389606;
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
CC   -!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; X12597; CAA31110.1; -; mRNA.
DR   EMBL; U51677; AAB08987.1; -; Genomic_DNA.
DR   EMBL; AY377859; AAQ91389.1; -; mRNA.
DR   EMBL; CR749614; CAH18408.1; -; mRNA.
DR   EMBL; CR456863; CAG33144.1; -; mRNA.
DR   EMBL; BT006940; AAP35586.1; -; mRNA.
DR   EMBL; BT020159; AAV38961.1; -; mRNA.
DR   EMBL; BC003378; AAH03378.1; -; mRNA.
DR   EMBL; BC030981; AAH30981.1; -; mRNA.
DR   EMBL; BC066889; AAH66889.1; -; mRNA.
DR   EMBL; BC067732; AAH67732.1; -; mRNA.
DR   PIR; S02826; S02826.
DR   HSSP; P07156; 1NHN.
DR   SMR; P09429; 1-83, 92-170.
DR   IntAct; P09429; -.
DR   Ensembl; ENSG00000189403; Homo sapiens.
DR   HGNC; HGNC:4983; HMGB1.
DR   H-InvDB; HIX0011209; -.
DR   MIM; 163905; -.
DR   GO; GO:0000793; C:condensed chromosome; IDA.
DR   GO; GO:0008301; F:DNA bending activity; TAS.
DR   GO; GO:0008134; F:transcription factor binding; TAS.
DR   GO; GO:0006288; P:base-excision repair, DNA ligation; IDA.
DR   GO; GO:0006310; P:DNA recombination; TAS.
DR   GO; GO:0006281; P:DNA repair; TAS.
DR   GO; GO:0006268; P:DNA unwinding; NAS.
DR   GO; GO:0006325; P:establishment and/or maintenance of chromat. . .; TAS.
DR   GO; GO:0017055; P:negative regulation of transcriptional prei. . .; IDA.
DR   GO; GO:0006357; P:regulation of transcription from RNA polyme. . .; IDA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
KW   Chromosomal protein; Direct protein sequencing; DNA-binding;
KW   Nuclear protein; Repeat.
FT   INIT_MET      0      0
FT   DNA_BIND      8     78       HMG box 1.
FT   DNA_BIND     94    162       HMG box 2.
FT   COMPBIAS    185    214       Asp/Glu-rich (acidic).
FT   CONFLICT    214    214       E -> D (in Ref. 5).
SQ   SEQUENCE   214 AA;  24763 MW;  B3C6A80FC7F0F433 CRC64;

  Query Match             100.0%;  Score 370;  DB 1;  Length 214;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-31;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 151

Qy         61 EKYEKDIAA 69
              |||||||||
Db        152 EKYEKDIAA 160


RESULT 8
HMG1_MOUSE
ID   HMG1_MOUSE     STANDARD;      PRT;   214 AA.
AC   P63158; P07155; P27109; P27428;
DT   01-APR-1988 (Rel. 07, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   High mobility group protein 1 (HMG-1) (High mobility group protein
DE   B1).
GN   Name=Hmgb1; Synonyms=Hmg-1, Hmg1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C3H/He;
RX   MEDLINE=92335012; PubMed=1630928;
RA   Yotov W.V., St Arnaud R.;
RT   "Nucleotide sequence of a mouse cDNA encoding the nonhistone
RT   chromosomal high mobility group protein-1 (HMG1).";
RL   Nucleic Acids Res. 20:3516-3516(1992).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=94235965; PubMed=8180479; DOI=10.1007/BF00292334;
RA   Pauken C.M., Nagle D.L., Bucan M., Lo C.W.;
RT   "Molecular cloning, expression analysis, and chromosomal localization
RT   of mouse Hmg1-containing sequences.";
RL   Mamm. Genome 5:91-99(1994).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=129/Sv; TISSUE=Liver;
RX   MEDLINE=95050689; PubMed=7961836;
RA   Ferrari S., Ronfani L., Calogero S., Bianchi M.;
RT   "The mouse gene coding for high mobility group 1 protein (HMG1).";
RL   J. Biol. Chem. 269:28803-28808(1994).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=AKR/J;
RA   Ghosh B.;
RL   Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
```

```
CC   -!- FUNCTION: Binds preferentially single-stranded DNA and unwinds
CC       double stranded DNA. Heparin-binding protein that has a role in
CC       the extension of neurite-type cytoplasmic processes in developing
CC       cells.
CC   -!- SUBCELLULAR LOCATION: Nuclear and also cytoplasmic, associated
CC       with the plasma membrane of filipodia in process-growing cells,
CC       and also deposited into the substrate-attached material.
CC   -!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
CC   -!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; Z11997; CAA78042.1; -; mRNA.
DR   EMBL; U00431; AAA20508.1; -; mRNA.
DR   EMBL; X80457; CAA56631.1; -; Genomic_DNA.
DR   EMBL; L38477; AAA57042.1; -; mRNA.
DR   EMBL; BC006586; AAH06586.1; -; mRNA.
DR   EMBL; BC008565; AAH08565.1; -; mRNA.
DR   EMBL; BC083067; AAH83067.1; -; mRNA.
DR   EMBL; BC085090; AAH85090.1; -; mRNA.
DR   PIR; I48688; I48688.
DR   SMR; P63158; 1-83, 92-170.
DR   MGI; MGI:96113; Hmgb1.
DR   GO; GO:0005615; C:extracellular space; IDA.
DR   GO; GO:0005634; C:nucleus; TAS.
DR   GO; GO:0030235; F:nitric-oxide synthase regulator activity; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0006809; P:nitric oxide biosynthesis; IDA.
DR   GO; GO:0006810; P:transport; IDA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
KW   Chromosomal protein; DNA-binding; Heparin-binding; Nuclear protein;
KW   Repeat.
FT   INIT_MET      0      0       By similarity.
FT   DNA_BIND      8     78       HMG box 1.
FT   DNA_BIND     94    162       HMG box 2.
FT   COMPBIAS    185    214       Asp/Glu-rich (acidic).
FT   CONFLICT    178    178       E -> V (in Ref. 4).
FT   CONFLICT    189    189       D -> E (in Ref. 3).
SQ   SEQUENCE   214 AA;  24763 MW;  B3C6A91FD6F1B133 CRC64;

  Query Match             100.0%;  Score 370;  DB 1;  Length 214;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-31;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 151

Qy         61 EKYEKDIAA 69
              |||||||||
Db        152 EKYEKDIAA 160


RESULT 9
HMG1_RAT
ID   HMG1_RAT       STANDARD;      PRT;   214 AA.
AC   P63159; P07155; P27109; P27428;
DT   01-APR-1988 (Rel. 07, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   High mobility group protein 1 (HMG-1) (High mobility group protein B1)
DE   (Amphoterin) (Heparin-binding protein p30).
GN   Name=Hmgb1; Synonyms=Hmg-1, Hmg1;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sprague-Dawley; TISSUE=Liver;
RX   MEDLINE=88067717; PubMed=3684582;
RA   Paonessa G., Frank R., Cortese R.;
RT   "Nucleotide sequence of rat liver HMG1 cDNA.";
RL   Nucleic Acids Res. 15:9077-9077(1987).
RN   [2]
RP   SEQUENCE REVISION.
RA   Bianchi M.;
RL   Submitted (DEC-1988) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.
RX   MEDLINE=91358468; PubMed=1885601;
RA   Merenmies J., Pihlaskari R., Laitinen J., Wartiovaara J., Rauvala H.;
RT   "30-kDa heparin-binding protein of brain (amphoterin) involved in
RT   neurite outgrowth. Amino acid sequence and localization in the
RT   filopodia of the advancing plasma membrane.";
RL   J. Biol. Chem. 266:16722-16729(1991).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Kidney, Prostate, and Testis;
RG   NIH - Mammalian Gene Collection (MGC) project;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   PROTEIN SEQUENCE OF 1-20.
RX   MEDLINE=89066894; PubMed=2461949; DOI=10.1083/jcb.107.6.2293;
RA   Rauvala H., Merenmies J., Pihlaskari R., Korkolainen M., Huhtala M.L.,
RA   Panula P.;
RT   "The adhesive and neurite-promoting molecule p30: analysis of the
RT   amino-terminal sequence and production of antipeptide antibodies that
RT   detect p30 at the surface of neuroblastoma cells and of brain
RT   neurons.";
RL   J. Cell Biol. 107:2293-2305(1988).
RN   [6]
RP   STRUCTURE BY NMR OF 87-164.
RX   MEDLINE=93223672; PubMed=8467791;
RA   Weir H.M., Kraulis P.J., Hill C.S., Raine A.R.C., Laue E.D.,
RA   Thomas J.O.;
RT   "Structure of the HMG box motif in the B-domain of HMG1.";
RL   EMBO J. 12:1311-1319(1993).
RN   [7]
RP   STRUCTURE BY NMR OF 1-83.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=96118376; PubMed=8527432;
RA   Hardman C.H., Broadhurst R.W., Raine A.R.C., Grasser K.D.,
RA   Thomas J.O., Laue E.D.;
RT   "Structure of the A-domain of HMG1 and its interaction with DNA as
RT   studied by heteronuclear three- and four-dimensional NMR
RT   spectroscopy.";
RL   Biochemistry 34:16596-16607(1995).
CC   -!- FUNCTION: Binds preferentially single-stranded DNA and unwinds
CC       double stranded DNA. Heparin-binding protein that has a role in
CC       the extension of neurite-type cytoplasmic processes in developing
CC       cells.
CC   -!- SUBCELLULAR LOCATION: Nuclear and also cytoplasmic, associated
CC       with the plasma membrane of filipodia in process-growing cells,
CC       and also deposited into the substrate-attached material.
CC   -!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
CC   -!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
CC   ---------------------------------------------------------------------
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; M64986; AAA40729.1; -; mRNA.
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DR   EMBL; Y00463; CAA68526.1; -; mRNA.
DR   EMBL; BC061779; AAH61779.1; -; mRNA.
DR   EMBL; BC081839; AAH81839.1; -; mRNA.
DR   EMBL; BC088402; AAH88402.1; -; mRNA.
DR   PIR; A41175; NSRTH1.
DR   PDB; 1AAB; NMR; @=1-83.
DR   PDB; 1CKT; X-ray; A=7-77.
DR   PDB; 1HME; NMR; @=88-164.
DR   PDB; 1HMF; NMR; @=88-164.
DR   SMR; P63159; 1-83, 92-170.
DR   Ensembl; ENSRNOG00000030351; Rattus norvegicus.
DR   RGD; 2802; Hmgb1.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
KW   3D-structure; Chromosomal protein; Direct protein sequencing;
KW   DNA-binding; Heparin-binding; Nuclear protein; Repeat.
FT   INIT_MET      0      0
FT   DNA_BIND      8     78       HMG box 1.
FT   DNA_BIND     94    162       HMG box 2.
FT   COMPBIAS    185    214       Asp/Glu-rich (acidic).
FT   HELIX        14     29
FT   TURN         31     32
FT   HELIX        37     49
FT   TURN         50     50
FT   TURN         53     55
FT   HELIX        57     74
FT   TURN         75     76
FT   HELIX       100    115
FT   TURN        117    118
FT   HELIX       121    134
FT   HELIX       137    158
FT   TURN        159    160
SQ   SEQUENCE   214 AA;  24763 MW;  B3C6A91FD6F1B133 CRC64;

  Query Match             100.0%;  Score 370;  DB 1;  Length 214;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-31;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
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Db         92 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 151

Qy         61 EKYEKDIAA 69
              |||||||||
Db        152 EKYEKDIAA 160


RESULT 10
Q5T7C3_HUMAN
ID   Q5T7C3_HUMAN PRELIMINARY;      PRT;   215 AA.
AC   Q5T7C3;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   High-mobility group box 1.
GN   Name=HMGB1; ORFNames=RP11-550P23.1-004;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Pelan S.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL353648; CAI15600.1; -; Genomic_DNA.
DR   GO; GO:0000785; C:chromatin; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
SQ   SEQUENCE   215 AA;  24894 MW;  8A868CF277D417B5 CRC64;

  Query Match             100.0%;  Score 370;  DB 2;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-31;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 152

Qy         61 EKYEKDIAA 69
              |||||||||
Db        153 EKYEKDIAA 161


RESULT 11
Q4R844_MACFA
ID   Q4R844_MACFA PRELIMINARY;      PRT;   215 AA.
AC   Q4R844;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Testis cDNA clone: QtsA-13487, similar to human high-mobility group
DE   box 1 (HMGB1),.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   International consortium for macaque cDNA sequencing, analysis;
RT   "DNA sequences of macaque genes expressed in brain or testis and its
RT   evolutionary implications.";
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Osada N., Hirata M., Tanuma R., Kusuda J., Hida M., Suzuki Y.,
RA   Sugano S., Gojobori T., Shen J.C.-K., Wu C.I., Hashimoto K.;
RT   "Substitution rate and structural divergence of 5'UTR evolution:
RT   Comparative analysis between human and cynomolgus monkey cDNAs.";
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB168615; BAE00728.1; -; mRNA.
SQ   SEQUENCE   215 AA;  24894 MW;  8A868CF277D417B5 CRC64;

  Query Match             100.0%;  Score 370;  DB 2;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-31;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 152

Qy         61 EKYEKDIAA 69
              |||||||||
Db        153 EKYEKDIAA 161


RESULT 12
O88611_SPAEH
ID   O88611_SPAEH PRELIMINARY;      PRT;   215 AA.
AC   O88611;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   High mobility group protein.
GN   Name=HMG1;
OS   Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Spalacinae; Nannospalax.
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OX   NCBI_TaxID=30637;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Lee K.-L.D., Lum H.-K., Nevo E.;
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF078817; AAC27650.2; -; Genomic_DNA.
DR   HSSP; P07156; 1NHN.
DR   SMR; O88611; 2-84, 93-171.
DR   GO; GO:0000785; C:chromatin; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
SQ   SEQUENCE   215 AA;  24905 MW;  64816B6FCF6033EA CRC64;

  Query Match             100.0%;  Score 370;  DB 2;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-31;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 152

Qy         61 EKYEKDIAA 69
              |||||||||
Db        153 EKYEKDIAA 161


RESULT 13
O88612_SPAEH
ID   O88612_SPAEH PRELIMINARY;      PRT;   215 AA.
AC   O88612;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   High mobility group protein.
GN   Name=HMG1;
OS   Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Spalacinae; Nannospalax.
OX   NCBI_TaxID=30637;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Lee K.-L.D., Lum H.-K., Nevo E.;
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF078818; AAC27651.1; -; Genomic_DNA.
DR   HSSP; P07156; 1NHN.
DR   SMR; O88612; 2-84, 93-171.
DR   GO; GO:0000785; C:chromatin; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
SQ   SEQUENCE   215 AA;  24923 MW;  1C6FB6845CA1E6C8 CRC64;

  Query Match             100.0%;  Score 370;  DB 2;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-31;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 152

Qy         61 EKYEKDIAA 69
              |||||||||
Db        153 EKYEKDIAA 161


RESULT 14
Q9QWY6_SPAEH
ID   Q9QWY6_SPAEH PRELIMINARY;      PRT;   215 AA.
AC   Q9QWY6;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   High mobility group protein.
GN   Name=HMG1;
OS   Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Spalacinae; Nannospalax.
OX   NCBI_TaxID=30637;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Lee K.-L.D., Lum H.-K., Nevo E.;
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF078819; AAC27652.1; -; Genomic_DNA.
DR   HSSP; P07156; 1NHN.
DR   SMR; Q9QWY6; 2-84, 93-171.
DR   GO; GO:0000785; C:chromatin; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
SQ   SEQUENCE   215 AA;  24822 MW;  D20D659274B575B4 CRC64;

  Query Match             100.0%;  Score 370;  DB 2;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-31;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 152

Qy         61 EKYEKDIAA 69
              |||||||||
Db        153 EKYEKDIAA 161


RESULT 15
Q9QX40_SPAEH
ID   Q9QX40_SPAEH PRELIMINARY;      PRT;   215 AA.
AC   Q9QX40;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   High mobility group protein.
GN   Name=HMG1;
OS   Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Spalacinae; Nannospalax.
OX   NCBI_TaxID=30637;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Lee K.-L.D., Lum H.-K., Nevo E.;
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF078820; AAC27653.2; -; Genomic_DNA.
DR   HSSP; P07156; 1NHN.
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DR   SMR; Q9QX40; 2-84, 93-171.
DR   GO; GO:0000785; C:chromatin; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
SQ   SEQUENCE   215 AA;  24895 MW;  599FB8A6FDF41F17 CRC64;

  Query Match             100.0%;  Score 370;  DB 2;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-31;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 152

Qy         61 EKYEKDIAA 69
              |||||||||
Db        153 EKYEKDIAA 161


Search completed: April  6, 2006, 10:25:16
Job time : 82.4836 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

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Title: US-10-717-984-5
Perfect score: 370
Sequence: 1 NAPKRPPSAFFLFCSEYRPK.....QPYEKKAAKLKEKYEKDIAA 69

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	370	100.0	214	2	US-09-538-092-883	Sequence 883, App
2	370	100.0	214	2	US-09-214-881A-1	Sequence 1, Appli
3	370	100.0	214	2	US-09-214-881A-3	Sequence 3, Appli
4	365	98.6	214	2	US-09-214-881A-4	Sequence 4, Appli
5	365	98.6	214	2	US-09-214-881A-5	Sequence 5, Appli
6	356	96.2	213	2	US-09-949-016-10813	Sequence 10813, A
7	324	87.6	208	2	US-09-538-092-1018	Sequence 1018, Ap
8	324	87.6	208	2	US-09-214-881A-2	Sequence 2, Appli
9	324	87.6	209	2	US-09-214-881A-6	Sequence 6, Appli
10	324	87.6	209	2	US-09-214-881A-8	Sequence 8, Appli
11	324	87.6	320	2	US-09-949-016-10728	Sequence 10728, A
12	321	86.8	206	2	US-09-214-881A-9	Sequence 9, Appli
13	317	85.7	879	2	US-09-914-259-38	Sequence 38, Appl
14	300	81.1	201	2	US-09-214-881A-10	Sequence 10, Appl
15	294	79.5	200	2	US-09-702-705-324	Sequence 324, App
16	294	79.5	200	2	US-09-702-705-789	Sequence 789, App
17	294	79.5	200	2	US-09-736-457-324	Sequence 324, App
18	294	79.5	200	2	US-09-736-457-789	Sequence 789, App
19	294	79.5	200	2	US-09-614-124B-324	Sequence 324, App
20	294	79.5	200	2	US-09-614-124B-789	Sequence 789, App
21	294	79.5	200	2	US-09-671-325-324	Sequence 324, App
22	294	79.5	200	2	US-09-671-325-789	Sequence 789, App
23	294	79.5	200	2	US-09-589-184-324	Sequence 324, App
24	294	79.5	200	2	US-09-589-184-789	Sequence 789, App
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27	294	79.5	200	2	US-10-017-754-324	Sequence 324, App
28	294	79.5	200	2	US-10-017-754-789	Sequence 789, App
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31	294	79.5	200	2	US-09-519-642-324	Sequence 324, App
32	294	79.5	200	2	US-09-519-642-789	Sequence 789, App
33	294	79.5	207	2	US-09-702-705-1667	Sequence 1667, Ap
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37	294	79.5	207	2	US-09-658-824-1667	Sequence 1667, Ap
38	294	79.5	207	2	US-10-017-754-1667	Sequence 1667, Ap
39	294	79.5	207	2	US-10-017-754-1913	Sequence 1913, Ap
40	294	79.5	207	2	US-09-651-563-1667	Sequence 1667, Ap
41	294	79.5	208	2	US-09-214-881A-11	Sequence 11, Appl
42	294	79.5	228	2	US-09-949-016-10496	Sequence 10496, A
43	292	78.9	185	2	US-09-214-881A-7	Sequence 7, Appli
44	170	45.9	709	1	US-07-814-964-7	Sequence 7, Appli
45	170	45.9	709	1	US-08-258-442-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-538-092-883
; Sequence 883, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 883
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P09429
US-09-538-092-883

Query Match 100.0%; Score 370; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 3.1e-40;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
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Db         92 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 151

Qy         61 EKYEKDIAA 69
              |||||||||
Db        152 EKYEKDIAA 160
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RESULT 2
US-09-214-881A-1
; Sequence 1, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
; APPLICANT: Uesugi, Hiroko
; APPLICANT: Okazaki, Takahiro
; APPLICANT: Tanaka, Masao

```
;  APPLICANT:  Nakao, Kazuwa
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION:  DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE:  068383.0104
;  CURRENT APPLICATION NUMBER: US/09/214,881A
;  CURRENT FILING DATE:  1999-06-07
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 214
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-214-881A-1

  Query Match             100.0%;  Score 370;  DB 2;  Length 214;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-40;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 151

Qy         61 EKYEKDIAA 69
              |||||||||
Db        152 EKYEKDIAA 160


RESULT 3
US-09-214-881A-3
; Sequence 3, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
;  APPLICANT:  Ozaki, Shoichi
;  APPLICANT:  Sobajima, Junko
;  APPLICANT:  Uesugi, Hiroko
;  APPLICANT:  Okazaki, Takahiro
;  APPLICANT:  Tanaka, Masao
;  APPLICANT:  Nakao, Kazuwa
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION:  DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE:  068383.0104
;  CURRENT APPLICATION NUMBER: US/09/214,881A
;  CURRENT FILING DATE:  1999-06-07
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 214
;   TYPE: PRT
;   ORGANISM: Bos taurus
US-09-214-881A-3

  Query Match             100.0%;  Score 370;  DB 2;  Length 214;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-40;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 151

Qy         61 EKYEKDIAA 69
              |||||||||
Db        152 EKYEKDIAA 160


RESULT 4
US-09-214-881A-4
; Sequence 4, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
;  APPLICANT:  Ozaki, Shoichi
;  APPLICANT:  Sobajima, Junko
;  APPLICANT:  Uesugi, Hiroko
;  APPLICANT:  Okazaki, Takahiro
;  APPLICANT:  Tanaka, Masao
;  APPLICANT:  Nakao, Kazuwa
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION:  DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE:  068383.0104
;  CURRENT APPLICATION NUMBER: US/09/214,881A
;  CURRENT FILING DATE:  1999-06-07
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 214
;   TYPE: PRT
;   ORGANISM: Sus scrofa
US-09-214-881A-4

  Query Match             98.6%;  Score 365;  DB 2;  Length 214;
  Best Local Similarity   98.6%;  Pred. No. 1.4e-39;
  Matches   68;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db         92 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKHPYEKKAAKLK 151

Qy         61 EKYEKDIAA 69
              |||||||||
Db        152 EKYEKDIAA 160


RESULT 5
US-09-214-881A-5
; Sequence 5, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
;  APPLICANT:  Ozaki, Shoichi
;  APPLICANT:  Sobajima, Junko
;  APPLICANT:  Uesugi, Hiroko
;  APPLICANT:  Okazaki, Takahiro
;  APPLICANT:  Tanaka, Masao
;  APPLICANT:  Nakao, Kazuwa
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION:  DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE:  068383.0104
;  CURRENT APPLICATION NUMBER: US/09/214,881A
;  CURRENT FILING DATE:  1999-06-07
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 214
;   TYPE: PRT
;   ORGANISM: Rattus rattus
US-09-214-881A-5

  Query Match             98.6%;  Score 365;  DB 2;  Length 214;
  Best Local Similarity   98.6%;  Pred. No. 1.4e-39;
  Matches   68;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db         92 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKHPYEKKAAKLK 151

Qy         61 EKYEKDIAA 69
              |||||||||
Db        152 EKYEKDIAA 160
```

```
RESULT 6
US-09-949-016-10813
; Sequence 10813, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10813
;   LENGTH: 213
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-10813

  Query Match             96.2%;  Score 356;  DB 2;  Length 213;
  Best Local Similarity   97.1%;  Pred. No. 2.1e-38;
  Matches   67;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||| |||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db         95 NAPKRTPSAFFLFCSAYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 154

Qy         61 EKYEKDIAA 69
              |||||||||
Db        155 EKYEKDIAA 163


RESULT 7
US-09-538-092-1018
; Sequence 1018, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
;  APPLICANT: Giot, Loic
;  APPLICANT:  Mansfield, Traci A.
;  TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
;  FILE REFERENCE: 15966-542
;  CURRENT APPLICATION NUMBER: US/09/538,092
;  CURRENT FILING DATE:  2000-03-29
;  PRIOR APPLICATION NUMBER: 60/127,352
;  PRIOR FILING DATE: 1999-04-01
;  PRIOR APPLICATION NUMBER: 60/178,965
;  PRIOR FILING DATE: 2000-02-01
;  NUMBER OF SEQ ID NOS: 1387
;  SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1018
;   LENGTH: 208
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Polypeptide Accession Number P26583
US-09-538-092-1018

  Query Match             87.6%;  Score 324;  DB 2;  Length 208;
  Best Local Similarity   87.0%;  Pred. No. 3e-34;
  Matches   60;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              |||||||||||||||:||||| ||||||||| ||||||||:  :| |||||||:||||||
Db         92 NAPKRPPSAFFLFCSEHRPKIKSEHPGLSIGDTAKKLGEMWSEQSAKDKQPYEQKAAKLK 151

Qy         61 EKYEKDIAA 69
              |||||||||
Db        152 EKYEKDIAA 160


RESULT 8
US-09-214-881A-2
; Sequence 2, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
;  APPLICANT:  Ozaki, Shoichi
;  APPLICANT:  Sobajima, Junko
;  APPLICANT:  Uesugi, Hiroko
;  APPLICANT:  Okazaki, Takahiro
;  APPLICANT:  Tanaka, Masao
;  APPLICANT:  Nakao, Kazuwa
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION:  DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE:  068383.0104
;  CURRENT APPLICATION NUMBER: US/09/214,881A
;  CURRENT FILING DATE:  1999-06-07
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 208
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-214-881A-2

  Query Match             87.6%;  Score 324;  DB 2;  Length 208;
  Best Local Similarity   87.0%;  Pred. No. 3e-34;
  Matches   60;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              |||||||||||||||:||||| ||||||||| ||||||||:  :| |||||||:||||||
Db         92 NAPKRPPSAFFLFCSEHRPKIKSEHPGLSIGDTAKKLGEMWSEQSAKDKQPYEQKAAKLK 151

Qy         61 EKYEKDIAA 69
              |||||||||
Db        152 EKYEKDIAA 160


RESULT 9
US-09-214-881A-6
; Sequence 6, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
;  APPLICANT:  Ozaki, Shoichi
;  APPLICANT:  Sobajima, Junko
;  APPLICANT:  Uesugi, Hiroko
;  APPLICANT:  Okazaki, Takahiro
;  APPLICANT:  Tanaka, Masao
;  APPLICANT:  Nakao, Kazuwa
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION:  DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE:  068383.0104
;  CURRENT APPLICATION NUMBER: US/09/214,881A
;  CURRENT FILING DATE:  1999-06-07
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 209
;   TYPE: PRT
;   ORGANISM: Sus scrofa
US-09-214-881A-6

  Query Match             87.6%;  Score 324;  DB 2;  Length 209;
  Best Local Similarity   87.0%;  Pred. No. 3e-34;
  Matches   60;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;
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```
Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||||||||||||:||||| |||||||| |||||||:  :| ||||||:||||||
Db         92 NAPKRPPSAFFLFCSEHRPKIKSEHPGLSIGDTAKKLGEMWSEQSAKDKQPYEQKAAKLK 151

Qy         61 EKYEKDIAA 69
              |||||||||
Db        152 EKYEKDIAA 160


RESULT 10
US-09-214-881A-8
; Sequence 8, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
;  APPLICANT:  Ozaki, Shoichi
;  APPLICANT:  Sobajima, Junko
;  APPLICANT:  Uesugi, Hiroko
;  APPLICANT:  Okazaki, Takahiro
;  APPLICANT:  Tanaka, Masao
;  APPLICANT:  Nakao, Kazuwa
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION:  DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE:  068383.0104
;  CURRENT APPLICATION NUMBER: US/09/214,881A
;  CURRENT FILING DATE:  1999-06-07
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 209
;   TYPE: PRT
;   ORGANISM: Rattus rattus
US-09-214-881A-8

  Query Match            87.6%;  Score 324;  DB 2;  Length 209;
  Best Local Similarity  87.0%;  Pred. No. 3e-34;
  Matches   60;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||||||||||||:||||| |||||||| |||||||:  :| ||||||:||||||
Db         92 NAPKRPPSAFFLFCSEHRPKIKSEHPGLSIGDTAKKLGEMWSEQSAKDKQPYEQKAAKLK 151

Qy         61 EKYEKDIAA 69
              |||||||||
Db        152 EKYEKDIAA 160


RESULT 11
US-09-949-016-10728
; Sequence 10728, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10728
;   LENGTH: 320
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-10728

  Query Match            87.6%;  Score 324;  DB 2;  Length 320;
  Best Local Similarity  87.0%;  Pred. No. 5.1e-34;
  Matches   60;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||||||||||||:||||| |||||||| |||||||:  :| ||||||:||||||
Db        204 NAPKRPPSAFFLFCSEHRPKIKSEHPGLSIGDTAKKLGEMWSEQSAKDKQPYEQKAAKLK 263

Qy         61 EKYEKDIAA 69
              |||||||||
Db        264 EKYEKDIAA 272


RESULT 12
US-09-214-881A-9
; Sequence 9, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
;  APPLICANT:  Ozaki, Shoichi
;  APPLICANT:  Sobajima, Junko
;  APPLICANT:  Uesugi, Hiroko
;  APPLICANT:  Okazaki, Takahiro
;  APPLICANT:  Tanaka, Masao
;  APPLICANT:  Nakao, Kazuwa
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION:  DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE:  068383.0104
;  CURRENT APPLICATION NUMBER: US/09/214,881A
;  CURRENT FILING DATE:  1999-06-07
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 206
;   TYPE: PRT
;   ORGANISM: Gallus gallus
US-09-214-881A-9

  Query Match            86.8%;  Score 321;  DB 2;  Length 206;
  Best Local Similarity  85.5%;  Pred. No. 7.3e-34;
  Matches   59;  Conservative    5;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||||||||||||:||||| :|||||||| |||||||:  :| ||||||:||||||
Db         92 NAPKRPPSAFFLFCSEHRPKIKNDHPGLSIGDTAKKLGEMWSEQSAKDKQPYEQKAAKLK 151

Qy         61 EKYEKDIAA 69
              |||||||||
Db        152 EKYEKDIAA 160


RESULT 13
US-09-914-259-38
; Sequence 38, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
;  APPLICANT: Makowski, Lee
;  APPLICANT:  Hyman, Paul
;  APPLICANT:  Williams, Mark
;  TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
;  FILE REFERENCE: 8471-010-999
;  CURRENT APPLICATION NUMBER: US/09/914,259
;  CURRENT FILING DATE:  2000-11-21
;  NUMBER OF SEQ ID NOS: 180
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
;   LENGTH: 879
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-914-259-38
```

```
  Query Match             85.7%;  Score 317;  DB 2;  Length 879;
  Best Local Similarity   88.4%;  Pred. No. 1.5e-32;
  Matches   61;  Conservative    1;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||| |||||||||||||||||||| || |||  ||||||| ||| |||||||||
Db        767 NAPKRPPLAFFLFCSEYRPKIKGEHPGLSIDDVVKKLAGMWNNTAAADKQFYEKKAAKLK 826

Qy         61 EKYEKDIAA 69
              |||:|||||
Db        827 EKYKKDIAA 835


RESULT 14
US-09-214-881A-10
; Sequence 10, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
;  APPLICANT:  Ozaki, Shoichi
;  APPLICANT:  Sobajima, Junko
;  APPLICANT:  Uesugi, Hiroko
;  APPLICANT:  Okazaki, Takahiro
;  APPLICANT:  Tanaka, Masao
;  APPLICANT:  Nakao, Kazuwa
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION:  DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE:  068383.0104
;  CURRENT APPLICATION NUMBER: US/09/214,881A
;  CURRENT FILING DATE:  1999-06-07
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 201
;   TYPE: PRT
;   ORGANISM: Gallus gallus
US-09-214-881A-10

  Query Match             81.1%;  Score 300;  DB 2;  Length 201;
  Best Local Similarity   79.4%;  Pred. No. 3.9e-31;
  Matches   54;  Conservative    6;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              |||||||| |||||||:||||| :||:||||||||||||||| :  :|||| ||||||
Db         90 NAPKRPPSGFFLFCSEFRPKIKSTNPGISIGDVAKKLGEMWNNLSDGEKQPYNNKAAKLK 149

Qy         61 EKYEKDIA 68
              ||||||:|
Db        150 EKYEKDVA 157


RESULT 15
US-09-702-705-324
; Sequence 324, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  Lodes, Michael A.
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Vedvick, Tom
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Retter, Marc
;  APPLICANT:  Mannion, Jane
;  APPLICANT:  Fan, Liqun
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE:  210121.478C14
;  CURRENT APPLICATION NUMBER: US/09/702,705
;  CURRENT FILING DATE:  2000-10-30
;  NUMBER OF SEQ ID NOS:  1833
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 324
;   LENGTH: 200
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-702-705-324

  Query Match             79.5%;  Score 294;  DB 2;  Length 200;
  Best Local Similarity   79.4%;  Pred. No. 2.4e-30;
  Matches   54;  Conservative    5;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              |||||||| |||||||:||||| :||:|||||||||||||||    :||||  ||||||
Db         91 NAPKRPPSGFFLFCSEFRPKIKSTNPGISIGDVAKKLGEMWNNLNDSEKQPYITKAAKLK 150

Qy         61 EKYEKDIA 68
              ||||||:|
Db        151 EKYEKDVA 158


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GenCore version 5.1.7

OM protein - protein search, using sw model

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(without alignments)
439.516 Million cell updates/sec

Title: US-10-717-984-5
Perfect score: 370
Sequence: 1 NAPKRPPSAFFLFCSEYRPK.....QPYEKKAAKLKEKYEKDIAA 69

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	370	100.0	69	4	US-10-147-447-5	Sequence 5, Appli
2	370	100.0	69	4	US-10-300-072-5	Sequence 5, Appli
3	370	100.0	69	4	US-10-456-949-5	Sequence 5, Appli
4	370	100.0	69	4	US-10-456-947-5	Sequence 5, Appli
5	370	100.0	69	4	US-10-718-495-5	Sequence 5, Appli
6	370	100.0	69	4	US-10-717-984-5	Sequence 5, Appli
7	370	100.0	74	4	US-10-300-072-51	Sequence 51, Appl
8	370	100.0	74	4	US-10-456-947-37	Sequence 37, Appl
9	370	100.0	74	4	US-10-718-495-51	Sequence 51, Appl
10	370	100.0	74	4	US-10-717-984-51	Sequence 51, Appl
11	370	100.0	74	5	US-10-938-992-67	Sequence 67, Appl
12	370	100.0	74	5	US-10-938-992-76	Sequence 76, Appl
13	370	100.0	92	4	US-10-300-072-58	Sequence 58, Appl
14	370	100.0	92	4	US-10-456-947-43	Sequence 43, Appl
15	370	100.0	92	4	US-10-718-495-58	Sequence 58, Appl
16	370	100.0	92	4	US-10-717-984-58	Sequence 58, Appl
17	370	100.0	92	5	US-10-938-992-73	Sequence 73, Appl
18	370	100.0	98	4	US-10-424-599-211221	Sequence 211221,
19	370	100.0	128	3	US-09-925-300-1757	Sequence 1757, Ap
20	370	100.0	176	4	US-10-094-749-2948	Sequence 2948, Ap
21	370	100.0	180	5	US-10-938-992-36	Sequence 36, Appl
22	370	100.0	214	3	US-09-214-881A-1	Sequence 1, Appli
23	370	100.0	214	3	US-09-214-881A-3	Sequence 3, Appli
24	370	100.0	214	5	US-10-726-195-1	Sequence 1, Appli
25	370	100.0	214	5	US-10-726-195-3	Sequence 3, Appli
26	370	100.0	215	4	US-10-087-192-1446	Sequence 1446, Ap
27	370	100.0	215	4	US-10-147-447-1	Sequence 1, Appli
28	370	100.0	215	4	US-10-147-447-2	Sequence 2, Appli
29	370	100.0	215	4	US-10-300-072-1	Sequence 1, Appli
30	370	100.0	215	4	US-10-300-072-2	Sequence 2, Appli
31	370	100.0	215	4	US-10-456-949-1	Sequence 1, Appli
32	370	100.0	215	4	US-10-456-949-2	Sequence 2, Appli
33	370	100.0	215	4	US-10-456-947-1	Sequence 1, Appli
34	370	100.0	215	4	US-10-456-947-2	Sequence 2, Appli
35	370	100.0	215	4	US-10-718-495-1	Sequence 1, Appli
36	370	100.0	215	4	US-10-718-495-2	Sequence 2, Appli
37	370	100.0	215	4	US-10-717-984-1	Sequence 1, Appli
38	370	100.0	215	4	US-10-717-984-2	Sequence 2, Appli
39	370	100.0	215	5	US-10-868-577A-63	Sequence 63, Appl
40	370	100.0	215	5	US-10-868-549-22	Sequence 22, Appl
41	370	100.0	215	5	US-10-938-992-18	Sequence 18, Appl
42	370	100.0	215	5	US-10-938-992-38	Sequence 38, Appl
43	370	100.0	215	5	US-10-938-992-74	Sequence 74, Appl
44	370	100.0	220	4	US-10-087-192-1443	Sequence 1443, Ap
45	370	100.0	221	5	US-10-938-992-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1
US-10-147-447-5
; Sequence 5, Application US/10147447
; Publication No. US20030060410A1
; GENERAL INFORMATION:
; APPLICANT: Tracey, Kevin J.
; APPLICANT: Yang, Huan
; APPLICANT: Warren Jr., Howland Shaw
; APPLICANT: Fink, Mitchell P.
; TITLE OF INVENTION: Use of HMG Fragments as
; TITLE OF INVENTION: Anti-Inflammatory Agents
; FILE REFERENCE: 3268.1001-001
; CURRENT APPLICATION NUMBER: US/10/147,447
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/291,034
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-147-447-5

Query Match 100.0%; Score 370; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 5.5e-37;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60

Qy         61 EKYEKDIAA 69
              |||||||||
Db         61 EKYEKDIAA 69
```

RESULT 2
US-10-300-072-5
; Sequence 5, Application US/10300072
; Publication No. US20030144201A1
; GENERAL INFORMATION:
; APPLICANT: Kevin J. Tracey
; APPLICANT: Huan Yang
; APPLICANT: Howland Shaw Warren, Jr.
; APPLICANT: Mitchell P. Fink
; TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS ANTI-FLAMMATORY
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 3268.1001-005
; CURRENT APPLICATION NUMBER: US/10/300,072

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;  CURRENT FILING DATE:  2002-11-20
;  PRIOR APPLICATION NUMBER: US 10/147,447
;  PRIOR FILING DATE: 2002-05-15
;  PRIOR APPLICATION NUMBER: US 60/291,034
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 69
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-300-072-5

  Query Match             100.0%;  Score 370;  DB 4;  Length 69;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-37;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60

Qy         61 EKYEKDIAA 69
              |||||||||
Db         61 EKYEKDIAA 69


RESULT 3
US-10-456-949-5
; Sequence 5, Application US/10456949
; Publication No. US20040005316A1
; GENERAL INFORMATION:
;  APPLICANT: Kevin J. Tracey
;  APPLICANT:  Huan Yang
;  TITLE OF INVENTION: USE OF HMG FRAGMENTS AS
;  TITLE OF INVENTION:  ANTI-INFLAMMATORY AGENTS
;  FILE REFERENCE: 3268.1001-006
;  CURRENT APPLICATION NUMBER: US/10/456,949
;  CURRENT FILING DATE:  2003-06-06
;  PRIOR APPLICATION NUMBER: 10/147,447
;  PRIOR FILING DATE: 2002-05-15
;  PRIOR APPLICATION NUMBER: 60/291,034
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 69
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-456-949-5

  Query Match             100.0%;  Score 370;  DB 4;  Length 69;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-37;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60

Qy         61 EKYEKDIAA 69
              |||||||||
Db         61 EKYEKDIAA 69


RESULT 4
US-10-456-947-5
; Sequence 5, Application US/10456947
; Publication No. US20040053841A1
; GENERAL INFORMATION:
;  APPLICANT: Kevin J. Tracey
;  APPLICANT:  Huan Yang
;  TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN
;  TITLE OF INVENTION:  HMGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS
;  TITLE OF INVENTION:  ANTI-INFLAMMATORY AGENTS
;  FILE REFERENCE: 3268.1001-007
;  CURRENT APPLICATION NUMBER: US/10/456,947
;  CURRENT FILING DATE:  2003-06-06
;  PRIOR APPLICATION NUMBER: 10/147,447
;  PRIOR FILING DATE: 2002-05-15
;  PRIOR APPLICATION NUMBER: 60/291,034
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 69
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Mouse/ rat/ human
US-10-456-947-5

  Query Match             100.0%;  Score 370;  DB 4;  Length 69;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-37;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60

Qy         61 EKYEKDIAA 69
              |||||||||
Db         61 EKYEKDIAA 69


RESULT 5
US-10-718-495-5
; Sequence 5, Application US/10718495
; Publication No. US20040141948A1
; GENERAL INFORMATION:
;  APPLICANT: O'Keefe, Theresa L.
;  TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS
;  TITLE OF INVENTION:  ANTI-INFLAMMATORY AGENTS
;  FILE REFERENCE: 3258.1009-001
;  CURRENT APPLICATION NUMBER: US/10/718,495
;  CURRENT FILING DATE:  2003-11-12
;  PRIOR APPLICATION NUMBER: 60/427,841
;  PRIOR FILING DATE: 2002-11-20
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 69
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-718-495-5

  Query Match             100.0%;  Score 370;  DB 4;  Length 69;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-37;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60

Qy         61 EKYEKDIAA 69
              |||||||||
Db         61 EKYEKDIAA 69


RESULT 6
US-10-717-984-5
; Sequence 5, Application US/10717984
; Publication No. US20040156851A1
; GENERAL INFORMATION:
;  APPLICANT: Newman, Walter
;  TITLE OF INVENTION: HMGB1 COMBINATION THERAPIES
;  FILE REFERENCE: 3258.1008-001
;  CURRENT APPLICATION NUMBER: US/10/717,984
```

```
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,846
;  PRIOR FILING DATE: 2002-11-20
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 69
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-717-984-5

  Query Match            100.0%;  Score 370;  DB 4;  Length 69;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-37;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60

Qy         61 EKYEKDIAA 69
              |||||||||
Db         61 EKYEKDIAA 69


RESULT 7
US-10-300-072-51
; Sequence 51, Application US/10300072
; Publication No. US20030144201A1
; GENERAL INFORMATION:
;  APPLICANT: Kevin J. Tracey
;  APPLICANT:  Huan Yang
;  APPLICANT:  Howland Shaw Warren, Jr.
;  APPLICANT:  Mitchell P. Fink
;  TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS ANTI-FLAMMATORY
;  TITLE OF INVENTION:  AGENTS
;  FILE REFERENCE: 3268.1001-005
;  CURRENT APPLICATION NUMBER: US/10/300,072
;  CURRENT FILING DATE:  2002-11-20
;  PRIOR APPLICATION NUMBER: US 10/147,447
;  PRIOR FILING DATE: 2002-05-15
;  PRIOR APPLICATION NUMBER: US 60/291,034
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 51
;   LENGTH: 74
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-300-072-51

  Query Match            100.0%;  Score 370;  DB 4;  Length 74;
  Best Local Similarity   100.0%;  Pred. No. 6e-37;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 64

Qy         61 EKYEKDIAA 69
              |||||||||
Db         65 EKYEKDIAA 73


RESULT 8
US-10-456-947-37
; Sequence 37, Application US/10456947
; Publication No. US20040053841A1
; GENERAL INFORMATION:
;  APPLICANT: Kevin J. Tracey
;  APPLICANT:  Huan Yang
;  TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN
;  TITLE OF INVENTION:  HMGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS
;  TITLE OF INVENTION:  ANTI-INFLAMMATORY AGENTS
;  FILE REFERENCE: 3268.1001-007
;  CURRENT APPLICATION NUMBER: US/10/456,947
;  CURRENT FILING DATE:  2003-06-06
;  PRIOR APPLICATION NUMBER: 10/147,447
;  PRIOR FILING DATE: 2002-05-15
;  PRIOR APPLICATION NUMBER: 60/291,034
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37
;   LENGTH: 74
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-456-947-37

  Query Match            100.0%;  Score 370;  DB 4;  Length 74;
  Best Local Similarity   100.0%;  Pred. No. 6e-37;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 64

Qy         61 EKYEKDIAA 69
              |||||||||
Db         65 EKYEKDIAA 73


RESULT 9
US-10-718-495-51
; Sequence 51, Application US/10718495
; Publication No. US20040141948A1
; GENERAL INFORMATION:
;  APPLICANT: O'Keefe, Theresa L.
;  TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS
;  TITLE OF INVENTION:  ANTI-INFLAMMATORY AGENTS
;  FILE REFERENCE: 3258.1009-001
;  CURRENT APPLICATION NUMBER: US/10/718,495
;  CURRENT FILING DATE:  2003-11-12
;  PRIOR APPLICATION NUMBER: 60/427,841
;  PRIOR FILING DATE: 2002-11-20
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 51
;   LENGTH: 74
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-718-495-51

  Query Match            100.0%;  Score 370;  DB 4;  Length 74;
  Best Local Similarity   100.0%;  Pred. No. 6e-37;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 64

Qy         61 EKYEKDIAA 69
              |||||||||
Db         65 EKYEKDIAA 73


RESULT 10
US-10-717-984-51
; Sequence 51, Application US/10717984
; Publication No. US20040156851A1
; GENERAL INFORMATION:
;  APPLICANT: Newman, Walter
;  TITLE OF INVENTION: HMGB1 COMBINATION THERAPIES
;  FILE REFERENCE: 3258.1008-001
;  CURRENT APPLICATION NUMBER: US/10/717,984
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,846
```

```
;  PRIOR FILING DATE: 2002-11-20
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 51
;   LENGTH: 74
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-717-984-51

  Query Match            100.0%;  Score 370;  DB 4;  Length 74;
  Best Local Similarity   100.0%;  Pred. No. 6e-37;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 64

Qy         61 EKYEKDIAA 69
              |||||||||
Db         65 EKYEKDIAA 73


RESULT 11
US-10-938-992-67
; Sequence 67, Application US/10938992
; Publication No. US20050152903A1
; GENERAL INFORMATION:
;  APPLICANT: Newman, Walter
;  APPLICANT:  Qin, Shixin
;  APPLICANT:  O'Keefe, Theresa
;  APPLICANT:  Obar, Robert
;  TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1
;  FILE REFERENCE: 3258.1033-001
;  CURRENT APPLICATION NUMBER: US/10/938,992
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: 60/502,568
;  PRIOR FILING DATE: 2003-09-11
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 67
;   LENGTH: 74
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-938-992-67

  Query Match            100.0%;  Score 370;  DB 5;  Length 74;
  Best Local Similarity   100.0%;  Pred. No. 6e-37;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 64

Qy         61 EKYEKDIAA 69
              |||||||||
Db         65 EKYEKDIAA 73


RESULT 12
US-10-938-992-76
; Sequence 76, Application US/10938992
; Publication No. US20050152903A1
; GENERAL INFORMATION:
;  APPLICANT: Newman, Walter
;  APPLICANT:  Qin, Shixin
;  APPLICANT:  O'Keefe, Theresa
;  APPLICANT:  Obar, Robert
;  TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1
;  FILE REFERENCE: 3258.1033-001
;  CURRENT APPLICATION NUMBER: US/10/938,992
;  CURRENT FILING DATE:  2004-09-10
;  PRIOR APPLICATION NUMBER: 60/502,568
;  PRIOR FILING DATE: 2003-09-11
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 76
;   LENGTH: 74
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-938-992-76

  Query Match            100.0%;  Score 370;  DB 5;  Length 74;
  Best Local Similarity   100.0%;  Pred. No. 6e-37;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 64

Qy         61 EKYEKDIAA 69
              |||||||||
Db         65 EKYEKDIAA 73


RESULT 13
US-10-300-072-58
; Sequence 58, Application US/10300072
; Publication No. US20030144201A1
; GENERAL INFORMATION:
;  APPLICANT: Kevin J. Tracey
;  APPLICANT:  Huan Yang
;  APPLICANT:  Howland Shaw Warren, Jr.
;  APPLICANT:  Mitchell P. Fink
;  TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS ANTI-FLAMMATORY
;  TITLE OF INVENTION:  AGENTS
;  FILE REFERENCE: 3268.1001-005
;  CURRENT APPLICATION NUMBER: US/10/300,072
;  CURRENT FILING DATE:  2002-11-20
;  PRIOR APPLICATION NUMBER: US 10/147,447
;  PRIOR FILING DATE: 2002-05-15
;  PRIOR APPLICATION NUMBER: US 60/291,034
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 58
;   LENGTH: 92
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-300-072-58

  Query Match            100.0%;  Score 370;  DB 4;  Length 92;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-37;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 64

Qy         61 EKYEKDIAA 69
              |||||||||
Db         65 EKYEKDIAA 73


RESULT 14
US-10-456-947-43
; Sequence 43, Application US/10456947
; Publication No. US20040053841A1
; GENERAL INFORMATION:
;  APPLICANT: Kevin J. Tracey
;  APPLICANT:  Huan Yang
;  TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN
;  TITLE OF INVENTION:  HMGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS
;  TITLE OF INVENTION:  ANTI-INFLAMMATORY AGENTS
;  FILE REFERENCE: 3268.1001-007
;  CURRENT APPLICATION NUMBER: US/10/456,947
;  CURRENT FILING DATE:  2003-06-06
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;  PRIOR APPLICATION NUMBER: 10/147,447
;  PRIOR FILING DATE: 2002-05-15
;  PRIOR APPLICATION NUMBER: 60/291,034
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 43
;   LENGTH: 92
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-456-947-43

  Query Match             100.0%;  Score 370;  DB 4;  Length 92;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-37;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 64

Qy         61 EKYEKDIAA 69
              |||||||||
Db         65 EKYEKDIAA 73


RESULT 15
US-10-718-495-58
; Sequence 58, Application US/10718495
; Publication No. US20040141948A1
; GENERAL INFORMATION:
;  APPLICANT: O'Keefe, Theresa L.
;  TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS
;  TITLE OF INVENTION:  ANTI-INFLAMMATORY AGENTS
;  FILE REFERENCE: 3258.1009-001
;  CURRENT APPLICATION NUMBER: US/10/718,495
;  CURRENT FILING DATE:  2003-11-12
;  PRIOR APPLICATION NUMBER: 60/427,841
;  PRIOR FILING DATE: 2002-11-20
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 58
;   LENGTH: 92
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-718-495-58

  Query Match             100.0%;  Score 370;  DB 4;  Length 92;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-37;
  Matches   69;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 64

Qy         61 EKYEKDIAA 69
              |||||||||
Db         65 EKYEKDIAA 73


Search completed: April  6, 2006, 10:32:47
Job time : 66.5954 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 10:28:08 ; Search time 8.625 Seconds
(without alignments)
249.536 Million cell updates/sec

Title: US-10-717-984-5
Perfect score: 370
Sequence: 1 NAPKRPPSAFFLFCSEYRPK.....QPYEKKAAKLKEKYEKDIAA 69

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 184161

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /SIDS5/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /SIDS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /SIDS5/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	370	100.0	69	7	US-11-186-422-14	Sequence 14, Appl
2	370	100.0	215	6	US-10-821-234-1443	Sequence 1443, Ap
3	370	100.0	215	7	US-11-186-422-11	Sequence 11, Appl
4	370	100.0	215	7	US-11-186-422-12	Sequence 12, Appl
5	317	85.7	879	7	US-11-169-041-192	Sequence 192, App
6	279	75.4	169	6	US-10-821-234-1234	Sequence 1234, Ap
7	168.5	45.5	139	7	US-11-096-568A-26884	Sequence 26884, A
8	168.5	45.5	187	7	US-11-096-568A-26883	Sequence 26883, A
9	165	44.6	92	7	US-11-087-099-8838	Sequence 8838, Ap
10	164.5	44.5	141	7	US-11-087-099-3073	Sequence 3073, Ap
11	163	44.1	93	7	US-11-087-099-869	Sequence 869, App
12	163	44.1	93	7	US-11-087-099-9518	Sequence 9518, Ap
13	162.5	43.9	149	7	US-11-087-099-3510	Sequence 3510, Ap
14	162.5	43.9	149	7	US-11-172-740-1571	Sequence 1571, Ap
15	159.5	43.1	141	7	US-11-087-099-9185	Sequence 9185, Ap
16	157.5	42.6	139	7	US-11-096-568A-13611	Sequence 13611, A
17	157.5	42.6	142	7	US-11-087-099-4976	Sequence 4976, Ap
18	156	42.2	99	7	US-11-087-099-2564	Sequence 2564, Ap
19	156	42.2	99	7	US-11-087-099-10060	Sequence 10060, A
20	154.5	41.8	124	7	US-11-096-568A-9681	Sequence 9681, Ap
21	154.5	41.8	162	7	US-11-096-568A-9680	Sequence 9680, Ap
22	153	41.4	187	7	US-11-096-568A-32735	Sequence 32735, A
23	153	41.4	241	7	US-11-096-568A-32734	Sequence 32734, A
24	153	41.4	257	7	US-11-096-568A-32733	Sequence 32733, A
25	151.5	40.9	160	7	US-11-087-099-1105	Sequence 1105, Ap
26	151	40.8	446	7	US-11-087-099-370	Sequence 370, App
27	150.5	40.7	127	7	US-11-096-568A-15615	Sequence 15615, A
28	150.5	40.7	154	7	US-11-096-568A-15614	Sequence 15614, A
29	149.5	40.4	146	7	US-11-172-740-1569	Sequence 1569, Ap
30	148.5	40.1	106	7	US-11-087-099-7075	Sequence 7075, Ap
31	148.5	40.1	152	7	US-11-087-099-313	Sequence 313, App
32	148.5	40.1	152	7	US-11-172-740-1565	Sequence 1565, Ap
33	148.5	40.1	152	7	US-11-172-740-1566	Sequence 1566, Ap
34	145	39.2	108	7	US-11-087-099-6594	Sequence 6594, Ap
35	144.5	39.1	145	7	US-11-172-740-1572	Sequence 1572, Ap
36	143	38.6	473	6	US-10-542-161-1	Sequence 1, Appli
37	142	38.4	310	7	US-11-087-099-4210	Sequence 4210, Ap
38	142	38.4	487	7	US-11-124-368A-308	Sequence 308, App
39	142	38.4	487	7	US-11-124-368A-309	Sequence 309, App
40	142	38.4	526	7	US-11-124-368A-310	Sequence 310, App
41	141.5	38.2	165	7	US-11-096-568A-21033	Sequence 21033, A
42	141.5	38.2	212	7	US-11-096-568A-21032	Sequence 21032, A
43	141.5	38.2	234	7	US-11-096-568A-21031	Sequence 21031, A
44	140.5	38.0	154	7	US-11-087-099-2474	Sequence 2474, Ap
45	140.5	38.0	154	7	US-11-172-740-1570	Sequence 1570, Ap

ALIGNMENTS

RESULT 1
US-11-186-422-14
; Sequence 14, Application US/11186422
; Publication No. US20060057679A1
; GENERAL INFORMATION:
; APPLICANT: Critical Therapeutics, Inc.
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Luciano, Peter
; APPLICANT: Qin, Shixin
; TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
; FILE REFERENCE: 3258.1021-003
; CURRENT APPLICATION NUMBER: US/11/186,422
; CURRENT FILING DATE: 2005-07-20
; PRIOR APPLICATION NUMBER: 60/589,678
; PRIOR FILING DATE: 2004-07-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-186-422-14

Query Match 100.0%; Score 370; DB 7; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.6e-37;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60

Qy         61 EKYEKDIAA 69
              |||||||||
Db         61 EKYEKDIAA 69
```

RESULT 2
US-10-821-234-1443
; Sequence 1443, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234

; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1443
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1443

Query Match 100.0%; Score 370; DB 6; Length 215;
Best Local Similarity 100.0%; Pred. No. 6.3e-37;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 93 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 152

Qy 61 EKYEKDIAA 69
|||||||||
Db 153 EKYEKDIAA 161

RESULT 3
US-11-186-422-11
; Sequence 11, Application US/11186422
; Publication No. US20060057679A1
; GENERAL INFORMATION:
; APPLICANT: Critical Therapeutics, Inc.
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Luciano, Peter
; APPLICANT: Qin, Shixin
; TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
; FILE REFERENCE: 3258.1021-003
; CURRENT APPLICATION NUMBER: US/11/186,422
; CURRENT FILING DATE: 2005-07-20
; PRIOR APPLICATION NUMBER: 60/589,678
; PRIOR FILING DATE: 2004-07-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-186-422-11

Query Match 100.0%; Score 370; DB 7; Length 215;
Best Local Similarity 100.0%; Pred. No. 6.3e-37;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 93 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 152

Qy 61 EKYEKDIAA 69
|||||||||
Db 153 EKYEKDIAA 161

RESULT 4
US-11-186-422-12
; Sequence 12, Application US/11186422
; Publication No. US20060057679A1
; GENERAL INFORMATION:
; APPLICANT: Critical Therapeutics, Inc.
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Luciano, Peter
; APPLICANT: Qin, Shixin
; TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
; FILE REFERENCE: 3258.1021-003
; CURRENT APPLICATION NUMBER: US/11/186,422
; CURRENT FILING DATE: 2005-07-20
; PRIOR APPLICATION NUMBER: 60/589,678
; PRIOR FILING DATE: 2004-07-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-186-422-12

Query Match 100.0%; Score 370; DB 7; Length 215;
Best Local Similarity 100.0%; Pred. No. 6.3e-37;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 93 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 152

Qy 61 EKYEKDIAA 69
|||||||||
Db 153 EKYEKDIAA 161

RESULT 5
US-11-169-041-192
; Sequence 192, Application US/11169041
; Publication No. US20060019284A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
; TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
; TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 10001 NP
; CURRENT APPLICATION NUMBER: US/11/169,041
; CURRENT FILING DATE: 2005-06-28
; PRIOR APPLICATION NUMBER: 60/584,405
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 527
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 192
; LENGTH: 879
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-169-041-192

Query Match 85.7%; Score 317; DB 7; Length 879;
Best Local Similarity 88.4%; Pred. No. 7.4e-30;
Matches 61; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
||||||| |||||||||||||||||||| || ||| ||||||| ||| |||||||||
Db 767 NAPKRPPLAFFLFCSEYRPKIKGEHPGLSIDDVVKKLAGMWNNTAAADKQPYEKKAAKLK 826

Qy 61 EKYEKDIAA 69
|||:|||||
Db 827 EKYKKDIAA 835

RESULT 6
US-10-821-234-1234
; Sequence 1234, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047

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;  PRIOR FILING DATE: 2003-04-07
;  NUMBER OF SEQ ID NOS: 1704
;  SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1234
;   LENGTH: 169
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(169)
;   OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-821-234-1234

  Query Match             75.4%;  Score 279;  DB 6;  Length 169;
  Best Local Similarity   75.0%;  Pred. No. 3.7e-26;
  Matches   51;  Conservative    6;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              ||||||||||||||||||:|||||  |||||||||  ||||  |||:  :  ||||||::||  |
Db         80 NAPKRPPSAFFLFCSEHRPKIKSEHPGLSIGDTAKKLDEMWSEQSGQDKQPYEQEAAYAK 139

Qy         61 EKYEKDIA 68
              |:|  || |
Db        140 EEYGKDFA 147


RESULT 7
US-11-096-568A-26884
; Sequence 26884, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26884
;   LENGTH: 139
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(139)
;   OTHER INFORMATION: Ceres Seq. ID no. 13627626
US-11-096-568A-26884

  Query Match             45.5%;  Score 168.5;  DB 7;  Length 139;
  Best Local Similarity   48.4%;  Pred. No. 5e-13;
  Matches   31;  Conservative   13;  Mismatches   19;  Indels    1;  Gaps    1;

Qy          3 PKRPPSAFFLFCSEYRPKIKGEHPG-LSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKE 61
              |||||||||:| ||:| : : :|||  |:  |:|  || | : :  :||||  :| : |:
Db         34 PKRPPSAFFVFMSEFRQEYQAQHPGNKSVAAVSKAAGEKWRSMSEQEKQPYVDQAGQKKQ 93

Qy         62 KYEK 65
                |||
Db         94 DYEK 97


RESULT 8
US-11-096-568A-26883
; Sequence 26883, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26883
;   LENGTH: 187
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(187)
;   OTHER INFORMATION: Ceres Seq. ID no. 13627625
US-11-096-568A-26883

  Query Match             45.5%;  Score 168.5;  DB 7;  Length 187;
  Best Local Similarity   48.4%;  Pred. No. 7.1e-13;
  Matches   31;  Conservative   13;  Mismatches   19;  Indels    1;  Gaps    1;

Qy          3 PKRPPSAFFLFCSEYRPKIKGEHPG-LSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKE 61
              |||||||||:| ||:| : : :|||  |:  |:|  || | : :  :||||  :| : |:
Db         82 PKRPPSAFFVFMSEFRQEYQAQHPGNKSVAAVSKAAGEKWRSMSEQEKQPYVDQAGQKKQ 141

Qy         62 KYEK 65
                |||
Db        142 DYEK 145


RESULT 9
US-11-087-099-8838
; Sequence 8838, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
;  CURRENT FILING DATE:  2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 8838
;   LENGTH: 92
;   TYPE: PRT
;   ORGANISM: Candida albicans
US-11-087-099-8838

  Query Match             44.6%;  Score 165;  DB 7;  Length 92;
  Best Local Similarity   47.1%;  Pred. No. 8e-13;
  Matches   32;  Conservative   12;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              :||||  ||:  | :| |  :: |:||:| | | | ||| |    ::|| ||| ||   |
Db         17 DAPKRSLSAYMFFANENRDIVRAENPGISFGQVGKLLGEKWKALNSEDKLPYENKAEADK 76

Qy         61 EKYEKDIA 68
              ::|||: |
Db         77 KRYEKEKA 84


RESULT 10
US-11-087-099-3073
; Sequence 3073, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
;  CURRENT FILING DATE:  2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3073
;   LENGTH: 141
;   TYPE: PRT
;   ORGANISM: Canavalia gladiata
US-11-087-099-3073

  Query Match             44.5%;  Score 164.5;  DB 7;  Length 141;
  Best Local Similarity   47.1%;  Pred. No. 1.5e-12;
  Matches   33;  Conservative   12;  Mismatches   24;  Indels    1;  Gaps    1;
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```
Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHP-GLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKL 59
              | |||||||||:| ||:| : | |||   |:  | |  |: | : :  :| |:  :| |
Db         35 NKPKRPPSAFFVFMSEFREQYKKEHPTNKSVAVVGKAGGDKWKSLSDAEKAPFVARAEKK 94

Qy         60 KEKYEKDIAA 69
              ||:|:| | |
Db         95 KEEYDKSILA 104


RESULT 11
US-11-087-099-869
; Sequence 869, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
;  CURRENT FILING DATE:  2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 869
;   LENGTH: 93
;   TYPE: PRT
;   ORGANISM: Saccharomyces cerevisiae
US-11-087-099-869

  Query Match             44.1%;  Score 163;  DB 7;  Length 93;
  Best Local Similarity   45.5%;  Pred. No. 1.4e-12;
  Matches   30;  Conservative   12;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              |||||  ||:  | :| |  :: |:| :: | | ||||| |     ::||||| ||   |
Db         19 NAPKRALSAYMFFANENRDIVRSENPDITFGQVGKKLGEKWKALTPEEKQPYEAKAQADK 78

Qy         61 EKYEKD 66
              ::|| :
Db         79 KRYESE 84


RESULT 12
US-11-087-099-9518
; Sequence 9518, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
;  CURRENT FILING DATE:  2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9518
;   LENGTH: 93
;   TYPE: PRT
;   ORGANISM: Saccharomyces cerevisiae
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(93)
;   OTHER INFORMATION: unsure at all Xaa locations
US-11-087-099-9518

  Query Match             44.1%;  Score 163;  DB 7;  Length 93;
  Best Local Similarity   45.5%;  Pred. No. 1.4e-12;
  Matches   30;  Conservative   12;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLK 60
              |||||  ||:  | :| |  :: |:| :: | | ||||| |     ::||||| ||   |
Db         19 NAPKRALSAYMFFANENRDIVRSENPDITFGQVGKKLGEKWKALTPEEKQPYEAKAQADK 78

Qy         61 EKYEKD 66
              ::|| :
Db         79 KRYESE 84


RESULT 13
US-11-087-099-3510
; Sequence 3510, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
;  CURRENT FILING DATE:  2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3510
;   LENGTH: 149
;   TYPE: PRT
;   ORGANISM: Vicia faba
US-11-087-099-3510

  Query Match             43.9%;  Score 162.5;  DB 7;  Length 149;
  Best Local Similarity   44.3%;  Pred. No. 2.8e-12;
  Matches   31;  Conservative   14;  Mismatches   24;  Indels    1;  Gaps    1;

Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHP-GLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKL 59
              | |||||||||:| :::| : | :||   |:  | |  || | : : ::| ||  :| |
Db         43 NKPKRPPSAFFVFMADFREQYKKDHPNNKSVAAVGKACGEEWKSLSEEEKAPYVDRALKK 102

Qy         60 KEKYEKDIAA 69
              ||:||  : |
Db        103 KEEYEITLQA 112


RESULT 14
US-11-172-740-1571
; Sequence 1571, Application US/11172740
; Publication No. US20060057724A1
; GENERAL INFORMATION:
;  APPLICANT: MASCIA, Peter
;  APPLICANT:  ALEXANDROV, Nickolai
;  APPLICANT:  BROVER, Vyacheslav
;  TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR M
;  TITLE OF INVENTION:  PLANT CHARACTERISTICS AND PHENOTYPES
;  FILE REFERENCE: 2750-1602PUS2
;  CURRENT APPLICATION NUMBER: US/11/172,740
;  CURRENT FILING DATE:  2005-06-30
;  PRIOR APPLICATION NUMBER: 60/583,621
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/584,829
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/584,800
;  PRIOR FILING DATE: 2004-06-30
;  NUMBER OF SEQ ID NOS: 2523
; SEQ ID NO 1571
;   LENGTH: 149
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(149)
;   OTHER INFORMATION: Public GI no. 729737
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: Utility: Useful for increasing seed/fruit yield or modifying fruit
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: Utility: Useful for making ornamental plants with modified flowers
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: Utility: Useful for making ornamental plants with modified leaves
;   FEATURE:
;   NAME/KEY: misc_feature
```

; LOCATION:
; OTHER INFORMATION: Utility: Useful for making plants sterile and for genetic confine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for making plants with increased biomass
US-11-172-740-1571

  Query Match 43.9%; Score 162.5; DB 7; Length 149;
  Best Local Similarity 44.3%; Pred. No. 2.8e-12;
  Matches 31; Conservative 14; Mismatches 24; Indels 1; Gaps 1;

```
Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHP-GLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKL 59
              | |||||||||:| :::| : | :||   |:  | |  || | : : ::| ||  :| |
Db         43 NKPKRPPSAFFVFMADFREQYKKDHPNNKSVAAVGKACGEEWKSLSEEEKAPYVDRALKK 102

Qy         60 KEKYEKDIAA 69
              ||:||  : |
Db        103 KEEYEITLQA 112
```

RESULT 15
US-11-087-099-9185
; Sequence 9185, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9185
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Solanum tuberosum
US-11-087-099-9185

  Query Match 43.1%; Score 159.5; DB 7; Length 141;
  Best Local Similarity 44.3%; Pred. No. 6.1e-12;
  Matches 31; Conservative 13; Mismatches 25; Indels 1; Gaps 1;

```
Qy          1 NAPKRPPSAFFLFCSEYRPKIKGEHP-GLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKL 59
              | |||||||||:|  |:|   | :||   |:  | |  |: |   : ::| ||: || |
Db         34 NKPKRPPSAFFVFMEEFRKTYKEKHPNNKSVAVVGKAGGDKWKQLSDEEKAPYQAKAEKR 93

Qy         60 KEKYEKDIAA 69
              | :|:|:: |
Db         94 KAEYQKNMDA 103
```

Search completed: April 6, 2006, 10:33:31
Job time : 9.625 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 10:12:19 ; Search time 24.2763 Seconds
(without alignments)
361.981 Million cell updates/sec

Title: US-10-717-984-23
Perfect score: 110
Sequence: 1 FKDPNAPKRLPSAFFLFCSE 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	110	100.0	20	6	AAE35864	Aae35864 Human HMG
2	110	100.0	20	8	ADO25940	Ado25940 Tumour ne
3	110	100.0	20	8	ADO71499	Ado71499 Human hig
4	110	100.0	74	6	AAE35868	Aae35868 Human HMG
5	110	100.0	74	8	ADO25937	Ado25937 Human hig
6	110	100.0	74	8	ADO25958	Ado25958 High mobi
7	110	100.0	74	8	ADO71496	Ado71496 Human hig
8	110	100.0	74	8	ADO71529	Ado71529 Human hig
9	110	100.0	74	9	ADY85364	Ady85364 Human hig
10	110	100.0	74	9	ADY85333	Ady85333 High mobi
11	110	100.0	74	9	ADY85080	Ady85080 Human HMG
12	110	100.0	74	9	ADY85014	Ady85014 Human HMG
13	110	100.0	182	6	AAE35867	Aae35867 Human HMG
14	110	100.0	182	8	ADO25936	Ado25936 Human hig
15	110	100.0	182	8	ADO71495	Ado71495 Human hig
16	110	100.0	182	9	ADY85379	Ady85379 Human hig
17	110	100.0	213	8	ADP30030	Adp30030 Human sec
18	110	100.0	216	6	AAE35866	Aae35866 Human HMG
19	110	100.0	216	8	ADO25935	Ado25935 Wild type
20	110	100.0	216	8	ADO25941	Ado25941 Human HMG
21	110	100.0	216	8	ADO71494	Ado71494 Human hig
22	110	100.0	216	8	ADO71500	Ado71500 Human hig
23	110	100.0	216	9	ADY85335	Ady85335 High mobi
24	110	100.0	216	9	ADY85331	Ady85331 Human hig
25	110	100.0	216	9	ADY85012	Ady85012 Human HMG
26	103	93.6	74	8	ADO25961	Ado25961 High mobi
27	103	93.6	74	8	ADO25959	Ado25959 High mobi
28	103	93.6	74	8	ADO25934	Ado25934 High mobi
29	103	93.6	74	8	ADO71530	Ado71530 Human hig
30	103	93.6	74	8	ADO71527	Ado71527 Human hig
31	103	93.6	74	8	ADO71532	Ado71532 Human hig
32	103	93.6	74	9	ADY85367	Ady85367 Human hig
33	103	93.6	74	9	ADY85362	Ady85362 Human hig
34	103	93.6	74	9	ADY85365	Ady85365 Human hig
35	103	93.6	74	9	ADY85083	Ady85083 Human HMG
36	103	93.6	74	9	ADY85078	Ady85078 Human HMG
37	103	93.6	74	9	ADY85081	Ady85081 Human HMG
38	103	93.6	74	9	ADY85087	Ady85087 Human HMG
39	103	93.6	92	8	ADO25962	Ado25962 High mobi
40	103	93.6	92	8	ADO71534	Ado71534 Human hig
41	103	93.6	92	9	ADY85368	Ady85368 Human hig
42	103	93.6	92	9	ADY85084	Ady85084 Human HMG
43	103	93.6	121	3	AAB53515	Aab53515 Human col
44	103	93.6	128	3	AAB57179	Aab57179 Human pro
45	103	93.6	128	4	AAG75983	Aag75983 Human col

ALIGNMENTS

RESULT 1
AAE35864
ID AAE35864 standard; peptide; 20 AA.
XX
AC AAE35864;
XX
DT 17-JUN-2003 (first entry)
XX
DE Human HMG1 B box fragment #1.
XX
KW Human; high mobility group; HMG protein; HMG A box; HMG B box; asthma;
KW inflammatory cytokine; endotoxic shock; rheumatoid arthritis; hepatitis;
KW appendicitis; peptic ulcer; duodenal ulcer; Crohn's disease; meningitis;
KW allergy; immune complex disease; sinusitis; bronchitis; atherosclerosis;
KW emphysema; HIV infection; candidiasis; malaria; filariasis; myocarditis;
KW Hodgkin's disease; neuritis; dermatitis; myocardial ischaemia; diabetes;
KW Alzheimer's disease; Goodpasture's syndrome; graft-versus-host disease;
KW amoebiasis; multiple sclerosis; gout; cerebral infarction; peritonitis;
KW gene therapy; human immunodeficiency virus; HMGB1 protein.
XX
OS Homo sapiens.
XX
PN WO200292004-A2.
XX
PD 21-NOV-2002.
XX
PF 15-MAY-2002; 2002WO-US015329.
XX
PR 15-MAY-2001; 2001US-0291034P.
XX
PA (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
PA (GEHO) GEN HOSPITAL CORP.
PA (UYPI-) UNIV PITTSBURGH.
XX
PI Tracey KJ, Yang H, Warren HS, Fink MP;
XX
DR WPI; 2003-120594/11.
XX
PT New isolated polypeptide having a vertebrate HMG A box, useful for
PT inhibiting a condition associated with an activated inflammatory cytokine
PT cascade, e.g. endotoxic shock, myocardial infarction, asthma, HIV
PT infection, malaria and diabetes.
XX
PS Example 4; Page 45; 82pp; English.
XX
CC The invention relates to high mobility group (HMG) protein comprising DNA
CC binding motifs termed HMG A box and HMG B box. HMG A box or a non-

CC naturally occurring HMG A box inhibits the release of a pro-inflammatory
CC cytokine from a vertebrate cell. The methods and compositions of the
CC invention are useful for inhibiting a condition characterised by
CC activation of an inflammatory cytokine cascade such as endotoxic shock,
CC rheumatoid arthritis, appendicitis, peptic or duodenal ulcers, Crohn's
CC disease, peritonitis, hepatitis, asthma, allergy, immune complex disease,
CC sinusitis, bronchitis, emphysema, HIV infection, candidiasis, malaria,
CC filariasis, amoebiasis, dermatitis, atherosclerosis, Alzheimer's disease,
CC myocarditis, myocardial ischaemia, meningitis, multiple sclerosis, gout,
CC cerebral infarction, neuritis, Goodpasture's syndrome, graft-versus-host
CC disease, diabetes and Hodgkin's disease. The invention is useful in gene
CC therapy. The present sequence is human HMG1 (also termed as HMGB1) B box
CC fragment
XX
SQ Sequence 20 AA;

Query Match 100.0%; Score 110; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FKDPNAPKRLPSAFFLFCSE 20
||||||||||||||||||||
Db 1 FKDPNAPKRLPSAFFLFCSE 20

RESULT 2
ADO25940
ID ADO25940 standard; peptide; 20 AA.
XX
AC ADO25940;
XX
DT 26-AUG-2004 (first entry)
XX
DE Tumour necrosis factor stimulating peptide.
XX
KW cytostatic; gene therapy; vaccine; pharmaceutical composition;
KW HMGB B box; high mobility group; immune response; immunostimulation;
KW cancer; human; high mobility group box 1; HMG1; cytokine activity;
KW TNF stimulating; tumour necrosis factor stimulating.
XX
OS Synthetic.
XX
PN WO2004046338-A2.
XX
PD 03-JUN-2004.
XX
PF 19-NOV-2003; 2003WO-US036975.
XX
PR 20-NOV-2002; 2002US-0427848P.
XX
PA (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
XX
PI Tracey KJ;
XX
DR WPI; 2004-420625/39.
XX
PT New pharmaceutical composition comprises a polypeptide comprising an HMGB
PT B box or its functional variant, useful for stimulating or increasing an
PT immune response in an individual or for treating cancer in an individual.
XX
PS Example 4; SEQ ID NO 23; 68pp; English.
XX
CC The invention describes a pharmaceutical composition comprising a
CC polypeptide comprising an HMGB (high mobility group box) B box or its
CC functional variant to treat a disease or condition by increasing an
CC immune response in an individual administered with the pharmaceutical
CC composition. Also described are: an antibody attached to a polypeptide
CC comprising an HMGB B box or its functional variant; stimulating or
CC increasing an immune response in an individual in need of
CC immunostimulation; and treating cancer in an individual. The composition
CC is useful for stimulating or increasing an immune response in an
CC individual in need of immunostimulation or for treating cancer in an
CC individual. This is the amino acid sequence of tumour necrosis factor
CC (TNF) stimulating peptide based on amino acids 1-20 of the human high
CC mobility group box 1 (HMG1) protein.
XX
SQ Sequence 20 AA;

Query Match 100.0%; Score 110; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FKDPNAPKRLPSAFFLFCSE 20
||||||||||||||||||||
Db 1 FKDPNAPKRLPSAFFLFCSE 20

RESULT 3
ADO71499
ID ADO71499 standard; peptide; 20 AA.
XX
AC ADO71499;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human high mobility group box 1 (HMGB1) B box protein active fragment #2.
XX
KW Human; high mobility group box 1 B box; HMGB1 B box; HMGB; HMGB A box;
KW HMGB B box; proinflammatory cytokine; weight loss; obesity; inflammation;
KW inflammatory cytokine cascade; sepsis; allograft rejection;
KW rheumatoid arthritis; asthma; lupus; adult respiratory distress syndrome;
KW chronic obstructive pulmonary disease; psoriasis; pancreatitis;
KW peritonitis; burn; myocardial ischaemia; organic ischaemia;
KW reperfusion ischaemia; Behcet's disease; graft-versus-host disease;
KW Crohn's disease; ulcerative colitis; multiple sclerosis; cachexia.
XX
OS Homo sapiens.
XX
PN WO2004046345-A2.
XX
PD 03-JUN-2004.
XX
PF 20-NOV-2003; 2003WO-US037507.
XX
PR 20-NOV-2002; 2002US-0427841P.
PR 20-NOV-2002; 2002US-0427846P.
XX
PA (CRIT-) CRITICAL THERAPEUTICS INC.
XX
PI Newman W, O'keefe TL;
XX
DR WPI; 2004-420628/39.
XX
PT New high mobility group box proteins, useful in treating obesity, sepsis,
PT rheumatoid arthritis, asthma, psoriasis, burns, myocardial ischemia,
PT Behcet's disease, ulcerative colitis, multiple sclerosis, or cachexia.
XX
PS Claim 33; SEQ ID NO 23; 113pp; English.
XX
CC The invention relates to a polypeptide comprising a high mobility group
CC box protein (HMGB) A or B box. The HMGB A or B box can inhibit release of
CC a proinflammatory cytokine from a cell treated with an HMGB protein. The
CC invention also relates to a purified preparation of antibodies that
CC specifically bind to the HMGB B box but do not specifically bind to non-B
CC box epitopes of HMGB, where the antibodies can inhibit release of a
CC proinflammatory cytokine from a cell treated with HMGB, a method for
CC effecting weight loss or treating obesity in a patient, a method of
CC determining whether a compound inhibits inflammation, a pharmaceutical
CC composition comprising an HMGB protein or an antibody that binds to the
CC protein, an agent that inhibits TNF biological activity and a method of
CC treating a condition in a patient characterised by activation of an
CC inflammatory cytokine cascade. Effecting weight loss or treating obesity
CC in a patient comprises administering to the patient an amount of the
CC polypeptide. The polypeptide, antibodies, composition and methods are
CC useful in treating obesity and conditions characterised by activation of
CC an inflammatory cytokine cascade, e.g. sepsis, allograft rejection,

CC rheumatoid arthritis, asthma, lupus, adult respiratory distress syndrome,
CC chronic obstructive pulmonary disease, psoriasis, pancreatitis,
CC peritonitis, burns, myocardial ischaemia, organic ischaemia, reperfusion
CC ischaemia, Behcet's disease, graft-versus-host disease, Crohn's disease,
CC ulcerative colitis, multiple sclerosis or cachexia. This sequence
CC represents a human HMGB1 B box polypeptide active fragment of the
CC invention.
XX
SQ Sequence 20 AA;

Query Match 100.0%; Score 110; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FKDPNAPKRLPSAFFLFCSE 20
||||||||||||||||||||
Db 1 FKDPNAPKRLPSAFFLFCSE 20

RESULT 4
AAE35868
ID AAE35868 standard; protein; 74 AA.
XX
AC AAE35868;
XX
DT 17-JUN-2003 (first entry)
XX
DE Human HMG1 protein mutant #2.
XX
KW Human; high mobility group; HMG protein; HMG A box; HMG B box; asthma;
KW inflammatory cytokine; endotoxic shock; rheumatoid arthritis; hepatitis;
KW appendicitis; peptic ulcer; duodenal ulcer; Crohn's disease; meningitis;
KW allergy; immune complex disease; sinusitis; bronchitis; atherosclerosis;
KW emphysema; HIV infection; candidiasis; malaria; filariasis; myocarditis;
KW Hodgkin's disease; neuritis; dermatitis; myocardial ischaemia; diabetes;
KW Alzheimer's disease; Goodpasture's syndrome; graft-versus-host disease;
KW amoebiasis; multiple sclerosis; gout; cerebral infarction; peritonitis;
KW gene therapy; human immunodeficiency virus; HMGB1 protein; mutant;
KW mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200292004-A2.
XX
PD 21-NOV-2002.
XX
PF 15-MAY-2002; 2002WO-US015329.
XX
PR 15-MAY-2001; 2001US-0291034P.
XX
PA (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
PA (GEHO) GEN HOSPITAL CORP.
PA (UYPI-) UNIV PITTSBURGH.
XX
PI Tracey KJ, Yang H, Warren HS, Fink MP;
XX
DR WPI; 2003-120594/11.
XX
PT New isolated polypeptide having a vertebrate HMG A box, useful for
PT inhibiting a condition associated with an activated inflammatory cytokine
PT cascade, e.g. endotoxic shock, myocardial infarction, asthma, HIV
PT infection, malaria and diabetes.
XX
PS Example 1; Page 37; 82pp; English.
XX
CC The invention relates to high mobility group (HMG) protein comprising DNA
CC binding motifs termed HMG A box and HMG B box. HMG A box or a non-
CC naturally occurring HMG A box inhibits the release of a pro-inflammatory
CC cytokine from a vertebrate cell. The methods and compositions of the
CC invention are useful for inhibiting a condition characterised by
CC activation of an inflammatory cytokine cascade such as endotoxic shock,
CC rheumatoid arthritis, appendicitis, peptic or duodenal ulcers, Crohn's
CC disease, peritonitis, hepatitis, asthma, allergy, immune complex disease,
CC sinusitis, bronchitis, emphysema, HIV infection, candidiasis, malaria,
CC filariasis, amoebiasis, dermatitis, atherosclerosis, Alzheimer's disease,
CC myocarditis, myocardial ischaemia, meningitis, multiple sclerosis, gout,
CC cerebral infarction, neuritis, Goodpasture's syndrome, graft-versus-host
CC disease, diabetes and Hodgkin's disease. The invention is useful in gene
CC therapy. The present sequence is human HMG1 (also termed as HMGB1)
CC protein (B box) mutant
XX
SQ Sequence 74 AA;

Query Match 100.0%; Score 110; DB 6; Length 74;
Best Local Similarity 100.0%; Pred. No. 8.9e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FKDPNAPKRLPSAFFLFCSE 20
||||||||||||||||||||
Db 1 FKDPNAPKRLPSAFFLFCSE 20

RESULT 5
ADO25937
ID ADO25937 standard; protein; 74 AA.
XX
AC ADO25937;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human high mobility group box 1 B-box mutant.
XX
KW cytostatic; gene therapy; vaccine; pharmaceutical composition;
KW HMGB B box; high mobility group; immune response; immunostimulation;
KW cancer; human; high mobility group box 1; HMG1; cytokine activity;
KW mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2004046338-A2.
XX
PD 03-JUN-2004.
XX
PF 19-NOV-2003; 2003WO-US036975.
XX
PR 20-NOV-2002; 2002US-0427848P.
XX
PA (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
XX
PI Tracey KJ;
XX
DR WPI; 2004-420625/39.
XX
PT New pharmaceutical composition comprises a polypeptide comprising an HMGB
PT B box or its functional variant, useful for stimulating or increasing an
PT immune response in an individual or for treating cancer in an individual.
XX
PS Example 1; SEQ ID NO 20; 68pp; English.
XX
CC The invention describes a pharmaceutical composition comprising a
CC polypeptide comprising an HMGB (high mobility group box) B box or its
CC functional variant to treat a disease or condition by increasing an
CC immune response in an individual administered with the pharmaceutical
CC composition. Also described are: an antibody attached to a polypeptide
CC comprising an HMGB B box or its functional variant; stimulating or
CC increasing an immune response in an individual in need of
CC immunostimulation; and treating cancer in an individual. The composition
CC is useful for stimulating or increasing an immune response in an
CC individual in need of immunostimulation or for treating cancer in an
CC individual. This is the amino acid sequence of a human high mobility
CC group box 1 (HMG1) B box mutant.
XX
SQ Sequence 74 AA;

```
  Query Match           100.0%;  Score 110;  DB 8;  Length 74;
  Best Local Similarity  100.0%;  Pred. No. 8.9e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              ||||||||||||||||||||
Db          1 FKDPNAPKRLPSAFFLFCSE 20


RESULT 6
ADO25958
ID   ADO25958 standard; peptide; 74 AA.
XX
AC   ADO25958;
XX
DT   26-AUG-2004  (first entry)
XX
DE   High mobility group box 1 B box fragment seqid 41.
XX
KW   cytostatic; gene therapy; vaccine; pharmaceutical composition;
KW   HMGB B box; high mobility group; immune response; immunostimulation;
KW   cancer; human; high mobility group box 1; HMG1; cytokine activity; B box.
XX
OS   Homo sapiens.
XX
PN   WO2004046338-A2.
XX
PD   03-JUN-2004.
XX
PF   19-NOV-2003; 2003WO-US036975.
XX
PR   20-NOV-2002; 2002US-0427848P.
XX
PA   (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
XX
PI   Tracey KJ;
XX
DR   WPI; 2004-420625/39.
XX
PT   New pharmaceutical composition comprises a polypeptide comprising an HMGB
PT   B box or its functional variant, useful for stimulating or increasing an
PT   immune response in an individual or for treating cancer in an individual.
XX
PS   Disclosure; SEQ ID NO 41; 68pp; English.
XX
CC   The invention describes a pharmaceutical composition comprising a
CC   polypeptide comprising an HMGB (high mobility group box) B box or its
CC   functional variant to treat a disease or condition by increasing an
CC   immune response in an individual administered with the pharmaceutical
CC   composition. Also described are: an antibody attached to a polypeptide
CC   comprising an HMGB B box or its functional variant; stimulating or
CC   increasing an immune response in an individual in need of
CC   immunostimulation; and treating cancer in an individual. The composition
CC   is useful for stimulating or increasing an immune response in an
CC   individual in need of immunostimulation or for treating cancer in an
CC   individual. This is the amino acid sequence of human high mobility group
CC   box 1 (HMG1) B box biologically active fragment.
XX
SQ   Sequence 74 AA;

  Query Match           100.0%;  Score 110;  DB 8;  Length 74;
  Best Local Similarity  100.0%;  Pred. No. 8.9e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              ||||||||||||||||||||
Db          1 FKDPNAPKRLPSAFFLFCSE 20


RESULT 7
ADO71496
ID   ADO71496 standard; protein; 74 AA.
XX
AC   ADO71496;
XX
DT   26-AUG-2004  (first entry)
XX
DE   Human high mobility group box 1 (HMGB1) mutant protein #2.
XX
KW   Human; high mobility group box 1; HMGB1; HMGB; HMGB A box; HMGB B box;
KW   proinflammatory cytokine; weight loss; obesity; inflammation;
KW   inflammatory cytokine cascade; sepsis; allograft rejection;
KW   rheumatoid arthritis; asthma; lupus; adult respiratory distress syndrome;
KW   chronic obstructive pulmonary disease; psoriasis; pancreatitis;
KW   peritonitis; burn; myocardial ischaemia; organic ischaemia;
KW   reperfusion ischaemia; Behcet's disease; graft-versus-host disease;
KW   Crohn's disease; ulcerative colitis; multiple sclerosis; cachexia;
KW   mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2004046345-A2.
XX
PD   03-JUN-2004.
XX
PF   20-NOV-2003; 2003WO-US037507.
XX
PR   20-NOV-2002; 2002US-0427841P.
PR   20-NOV-2002; 2002US-0427846P.
XX
PA   (CRIT-) CRITICAL THERAPEUTICS INC.
XX
PI   Newman W,  O'keefe TL;
XX
DR   WPI; 2004-420628/39.
XX
PT   New high mobility group box proteins, useful in treating obesity, sepsis,
PT   rheumatoid arthritis, asthma, psoriasis, burns, myocardial ischemia,
PT   Behcet's disease, ulcerative colitis, multiple sclerosis, or cachexia.
XX
PS   Example 1; SEQ ID NO 20; 113pp; English.
XX
CC   The invention relates to a polypeptide comprising a high mobility group
CC   box protein (HMGB) A or B box. The HMGB A or B box can inhibit release of
CC   a proinflammatory cytokine from a cell treated with an HMGB protein. The
CC   invention also relates to a purified preparation of antibodies that
CC   specifically bind to the HMGB B box but do not specifically bind to non-B
CC   box epitopes of HMGB, where the antibodies can inhibit release of a
CC   proinflammatory cytokine from a cell treated with HMGB, a method for
CC   effecting weight loss or treating obesity in a patient, a method of
CC   determining whether a compound inhibits inflammation, a pharmaceutical
CC   composition comprising an HMGB protein or an antibody that binds to the
CC   protein, an agent that inhibits TNF biological activity and a method of
CC   treating a condition in a patient characterised by activation of an
CC   inflammatory cytokine cascade. Effecting weight loss or treating obesity
CC   in a patient comprises administering to the patient an amount of the
CC   polypeptide. The polypeptide, antibodies, composition and methods are
CC   useful in treating obesity and conditions characterised by activation of
CC   an inflammatory cytokine cascade, e.g. sepsis, allograft rejection,
CC   rheumatoid arthritis, asthma, lupus, adult respiratory distress syndrome,
CC   chronic obstructive pulmonary disease, psoriasis, pancreatitis,
CC   peritonitis, burns, myocardial ischaemia, organic ischaemia, reperfusion
CC   ischaemia, Behcet's disease, graft-versus-host disease, Crohn's disease,
CC   ulcerative colitis, multiple sclerosis or cachexia. This sequence
CC   represents a human HMGB1 mutant polypeptide of the invention.
XX
SQ   Sequence 74 AA;

  Query Match           100.0%;  Score 110;  DB 8;  Length 74;
  Best Local Similarity  100.0%;  Pred. No. 8.9e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              ||||||||||||||||||||
Db          1 FKDPNAPKRLPSAFFLFCSE 20
```

```
RESULT 8
ADO71529
ID   ADO71529 standard; protein; 74 AA.
XX
AC   ADO71529;
XX
DT   26-AUG-2004  (first entry)
XX
DE   Human high mobility group box (HMGB) B box protein #3.
XX
KW   Human; high mobility group box B box; HMGB; HMGB A box; HMGB B box;
KW   proinflammatory cytokine; weight loss; obesity; inflammation;
KW   inflammatory cytokine cascade; sepsis; allograft rejection;
KW   rheumatoid arthritis; asthma; lupus; adult respiratory distress syndrome;
KW   chronic obstructive pulmonary disease; psoriasis; pancreatitis;
KW   peritonitis; burn; myocardial ischaemia; organic ischaemia;
KW   reperfusion ischaemia; Behcet's disease; graft-versus-host disease;
KW   Crohn's disease; ulcerative colitis; multiple sclerosis; cachexia.
XX
OS   Homo sapiens.
XX
PN   WO2004046345-A2.
XX
PD   03-JUN-2004.
XX
PF   20-NOV-2003; 2003WO-US037507.
XX
PR   20-NOV-2002; 2002US-0427841P.
PR   20-NOV-2002; 2002US-0427846P.
XX
PA   (CRIT-) CRITICAL THERAPEUTICS INC.
XX
PI   Newman W,  O'keefe TL;
XX
DR   WPI; 2004-420628/39.
XX
PT   New high mobility group box proteins, useful in treating obesity, sepsis,
PT   rheumatoid arthritis, asthma, psoriasis, burns, myocardial ischemia,
PT   Behcet's disease, ulcerative colitis, multiple sclerosis, or cachexia.
XX
PS   Disclosure; SEQ ID NO 53; 113pp; English.
XX
CC   The invention relates to a polypeptide comprising a high mobility group
CC   box protein (HMGB) A or B box. The HMGB A or B box can inhibit release of
CC   a proinflammatory cytokine from a cell treated with an HMGB protein. The
CC   invention also relates to a purified preparation of antibodies that
CC   specifically bind to the HMGB B box but do not specifically bind to non-B
CC   box epitopes of HMGB, where the antibodies can inhibit release of a
CC   proinflammatory cytokine from a cell treated with HMGB, a method for
CC   effecting weight loss or treating obesity in a patient, a method of
CC   determining whether a compound inhibits inflammation, a pharmaceutical
CC   composition comprising an HMGB protein or an antibody that binds to the
CC   protein, an agent that inhibits TNF biological activity and a method of
CC   treating a condition in a patient characterised by activation of an
CC   inflammatory cytokine cascade. Effecting weight loss or treating obesity
CC   in a patient comprises administering to the patient an amount of the
CC   polypeptide. The polypeptide, antibodies, composition and methods are
CC   useful in treating obesity and conditions characterised by activation of
CC   an inflammatory cytokine cascade, e.g. sepsis, allograft rejection,
CC   rheumatoid arthritis, asthma, lupus, adult respiratory distress syndrome,
CC   chronic obstructive pulmonary disease, psoriasis, pancreatitis,
CC   peritonitis, burns, myocardial ischaemia, organic ischaemia, reperfusion
CC   ischaemia, Behcet's disease, graft-versus-host disease, Crohn's disease,
CC   ulcerative colitis, multiple sclerosis or cachexia. This sequence
CC   represents a human HMGB B box polypeptide of the invention.
XX
SQ   Sequence 74 AA;

  Query Match           100.0%;  Score 110;  DB 8;  Length 74;
  Best Local Similarity  100.0%;  Pred. No. 8.9e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              ||||||||||||||||||||
Db          1 FKDPNAPKRLPSAFFLFCSE 20


RESULT 9
ADY85364
ID   ADY85364 standard; protein; 74 AA.
XX
AC   ADY85364;
XX
DT   02-JUN-2005  (first entry)
XX
DE   Human high mobility group box protein HMG1L10 B box.
XX
KW   High mobility group box; HMG1L10; immune disorder; infection;
KW   immunosuppressive; autoimmune disease; allergy; antiallergic;
KW   ulcerative colitis; antiinflammatory; antiulcer; gastrointestinal-gen.;
KW   Crohns disease; inflammation; asthma; antiasthmatic;
KW   rheumatoid arthritis; antirheumatic; antiarthritic; psoriasis;
KW   antipsoriatic; systemic lupus erythematosus; dermatological; antiulcer.
XX
OS   Unidentified.
XX
PN   WO2005025604-A2.
XX
PD   24-MAR-2005.
XX
PF   10-SEP-2004; 2004WO-US029540.
XX
PR   10-SEP-2003; 2003US-0502349P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
XX
PI   Warren HS,  Tracey KJ;
XX
DR   WPI; 2005-233421/24.
XX
PT   Treating an immune pathology in an individual comprises administering an
PT   amount of a high mobility group box (HMGB) polypeptide comprising a
PT   vertebrate or a non-naturally occurring HMGB A or B box, or its
PT   immunosuppressive fragment.
XX
PS   Disclosure; SEQ ID NO 39; 57pp; English.
XX
CC   The invention is based on the discovery that high mobility group box
CC   protein 1 (HMGB1, also known as high mobility group-1 or HMG1), when
CC   administered with an antigen, diminishes the antibody response to the
CC   administered antigen. HMGB1 has 2 DNA binding motifs, termed the A and B
CC   boxes. A claimed method of treating an immune pathology in an individual
CC   comprises administering a HMGB polypeptide comprising a vertebrate HMGB A
CC   box, a non-naturally-occurring HMGB A box, or an immunosuppressive
CC   fragment of the vertebrate or non-natural HMGB A box. The immune
CC   pathology is induced by the administration of a non-human antigen, non-
CC   self material (e.g. a cell or tissue such as bone marrow cells) or
CC   adjuvant to the individual, by the transplantation of an organ into the
CC   individual, or by infection from a microorganism. Claimed methods of
CC   protecting a subject against an immune pathology, inhibiting an immune
CC   pathology in an individual or decreasing an immune response to an
CC   administered non-human antigen comprise administering a HMGB polypeptide
CC   comprising a vertebrate HMGB A box, a non-naturally-occurring HMGB A box,
CC   or an immunosuppressive fragment of the vertebrate or non-natural A box.
CC   A claimed method of treating an autoimmune disorder in an individual
CC   comprises administering a HMGB polypeptide comprising a vertebrate HMGB A
CC   box, a non-naturally-occurring HMGB A box, or an immunosuppressive
CC   fragment of these, and a vertebrate or non-naturally-occurring HMGB B
CC   box. The HMGB polypeptide is preferably a HMGB1 peptide and may be
CC   truncated at the C-terminus. The autoimmune disease is allergy,
CC   ulcerative colitis, Crohn's disease, asthma, rheumatoid arthritis,
CC   psoriasis or systemic lupus erythematosus (all claimed). The present
CC   sequence is that of the B box of human HMG1L10, a HMGB protein.
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```
XX
SQ   Sequence 74 AA;

  Query Match             100.0%;  Score 110;  DB 9;  Length 74;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              ||||||||||||||||||||
Db          1 FKDPNAPKRLPSAFFLFCSE 20


RESULT 10
ADY85333
ID   ADY85333 standard; protein; 74 AA.
XX
AC   ADY85333;
XX
DT   02-JUN-2005  (first entry)
XX
DE   High mobility group box protein HMGB1 B box mutant.
XX
KW   High mobility group box; HMGB1; immune disorder; infection;
KW   immunosuppressive; autoimmune disease; allergy; antiallergic;
KW   ulcerative colitis; antiinflammatory; antiulcer; gastrointestinal-gen.;
KW   Crohns disease; inflammation; asthma; antiasthmatic;
KW   rheumatoid arthritis; antirheumatic; antiarthritic; psoriasis;
KW   antipsoriatic; systemic lupus erythematosus; dermatological; antiulcer;
KW   mutein.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Rattus sp.
OS   Synthetic.
XX
PN   WO2005025604-A2.
XX
PD   24-MAR-2005.
XX
PF   10-SEP-2004; 2004WO-US029540.
XX
PR   10-SEP-2003; 2003US-0502349P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
XX
PI   Warren HS,  Tracey KJ;
XX
DR   WPI; 2005-233421/24.
XX
PT   Treating an immune pathology in an individual comprises administering an
PT   amount of a high mobility group box (HMGB) polypeptide comprising a
PT   vertebrate or a non-naturally occurring HMGB A or B box, or its
PT   immunosuppressive fragment.
XX
PS   Example 1; SEQ ID NO 8; 57pp; English.
XX
CC   The invention is based on the discovery that high mobility group box
CC   protein 1 (HMGB1, also known as high mobility group-1 or HMG1), when
CC   administered with an antigen, diminishes the antibody response to the
CC   administered antigen. HMGB1 has 2 DNA binding motifs, termed the A and B
CC   boxes. A claimed method of treating an immune pathology in an individual
CC   comprises administering a HMGB polypeptide comprising a vertebrate HMGB A
CC   box, a non-naturally-occurring HMGB A box, or an immunosuppressive
CC   fragment of the vertebrate or non-natural HMGB A box. The immune
CC   pathology is induced by the administration of a non-human antigen, non-
CC   self material (e.g. a cell or tissue such as bone marrow cells) or
CC   adjuvant to the individual, by the transplantation of an organ into the
CC   individual, or by infection from a microorganism. Claimed methods of
CC   protecting a subject against an immune pathology, inhibiting an immune
CC   pathology in an individual or decreasing an immune response to an
CC   administered non-human antigen comprise administering a HMGB polypeptide
CC   comprising a vertebrate HMGB A box, a non-naturally-occurring HMGB A box,
CC   or an immunosuppressive fragment of the vertebrate or non-natural A box.
CC   A claimed method of treating an autoimmune disorder in an individual
CC   comprises administering a HMGB polypeptide comprising a vertebrate HMGB A
CC   box, a non-naturally-occurring HMGB A box, or an immunosuppressive
CC   fragment of these, and a vertebrate or non-naturally-occurring HMGB B
CC   box. The HMGB polypeptide is preferably a HMGB1 peptide and may be
CC   truncated at the C-terminus. The autoimmune disease is allergy,
CC   ulcerative colitis, Crohn's disease, asthma, rheumatoid arthritis,
CC   psoriasis or systemic lupus erythematosus (all claimed). The present
CC   sequence is that of a mutated B box of human, mouse and rat HMGB1
CC   proteins ADY85326-ADY85327, which was produced in an example from the
CC   invention.
XX
SQ   Sequence 74 AA;

  Query Match             100.0%;  Score 110;  DB 9;  Length 74;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              ||||||||||||||||||||
Db          1 FKDPNAPKRLPSAFFLFCSE 20


RESULT 11
ADY85080
ID   ADY85080 standard; protein; 74 AA.
XX
AC   ADY85080;
XX
DT   16-JUN-2005  (first entry)
XX
DE   Human HMGB1 A box.
XX
KW   High mobility group box; HMGB1; monoclonal antibody; antibody therapy;
KW   sepsis; antibacterial immunosuppressive; graft rejection; arthritis;
KW   antiarthritic; asthma; antiasthmatic; lupus erythematosus;
KW   antiinflammatory; inflammation; dermatological;
KW   respiratory distress syndrome; respiratory-gen.; psoriasis;
KW   antipsoriatic; chronic obstructive pulmonary disease; pancreatitis;
KW   peritonitis; burns; vulnerary; ischemia; vasotropic; Behcets disease;
KW   graft versus host disease; inflammatory bowel disease;
KW   gastrointestinal-gen.; multiple sclerosis neuroprotective; cachexia;
KW   anabolic; infection; musculoskeletal disease; immune disorder.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Rattus sp.
XX
PN   WO2005026209-A2.
XX
PD   24-MAR-2005.
XX
PF   10-SEP-2004; 2004WO-US029527.
XX
PR   11-SEP-2003; 2003US-0502568P.
XX
PA   (CRIT-) CRITICAL THERAPEUTICS INC.
XX
PI   Newman W,  Qin S,  Okeefe T,  Obar R;
XX
DR   WPI; 2005-233483/24.
XX
PT   New antibody or its antigen-binding fragment specific to a vertebrate
PT   high mobility group box (HMGB) A box that inhibits release of a
PT   proinflammatory cytokine from a cell treated with HMGB protein, useful
PT   for treating, e.g. sepsis.
XX
PS   Disclosure; SEQ ID NO 2; 123pp; English.
XX
CC   The invention provides antibodies, or their antigen-binding fragments,
CC   that bind to a vertebrate high mobility group box (HMGB) polypeptide, to
CC   methods of detecting and/or identifying an agent that binds to an HMGB
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CC   polypeptide, methods of treating a condition in a subject characterized
CC   by activation of an inflammatory cytokine cascade, and methods of
CC   detecting an HMGB polypeptide in a sample. The antibody (or antigen-
CC   binding fragment) binds to a vertebrate HMGB A box but does not
CC   specifically bind to non-A box epitopes of HMGB, and inhibits release of
CC   a proinflammatory cytokine from a vertebrate cell treated with an HMGB
CC   protein. A method of treating a condition characterized by activation of
CC   an inflammatory cytokine cascade comprises administering an antibody of
CC   the invention, or its antigen-binding fragment. The condition is selected
CC   from sepsis, allograft rejection, arthritis, asthma, lupus, adult
CC   respiratory distress syndrome, chronic obstructive pulmonary disease,
CC   psoriasis, pancreatitis, peritonitis, burns, ischemia, Behcet's disease,
CC   graft versus host disease, inflammatory bowel disease, multiple sclerosis
CC   and cachexia, especially sepsis, arthritis, or lupus. The present
CC   sequence is that of the A box of human HMGB1 ADY85012. An identical
CC   sequence is also found in rat and mouse HMGB1.
XX
SQ   Sequence 74 AA;

  Query Match             100.0%;  Score 110;  DB 9;  Length 74;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              ||||||||||||||||||||
Db          1 FKDPNAPKRLPSAFFLFCSE 20


RESULT 12
ADY85014
ID   ADY85014 standard; protein; 74 AA.
XX
AC   ADY85014;
XX
DT   16-JUN-2005  (first entry)
XX
DE   Human HMGB1 A box.
XX
KW   High mobility group box; HMGB1; monoclonal antibody; antibody therapy;
KW   sepsis; antibacterial immunosuppressive; graft rejection; arthritis;
KW   antiarthritic; asthma; antiasthmatic; lupus erythematosus;
KW   antiinflammatory; inflammation; dermatological;
KW   respiratory distress syndrome; respiratory-gen.; psoriasis;
KW   antipsoriatic; chronic obstructive pulmonary disease; pancreatitis;
KW   peritonitis; burns; vulnerary; ischemia; vasotropic; Behcets disease;
KW   graft versus host disease; inflammatory bowel disease;
KW   gastrointestinal-gen.; multiple sclerosis neuroprotective; cachexia;
KW   anabolic; infection; musculoskeletal disease; immune disorder.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Rattus sp.
XX
PN   WO2005026209-A2.
XX
PD   24-MAR-2005.
XX
PF   10-SEP-2004; 2004WO-US029527.
XX
PR   11-SEP-2003; 2003US-0502568P.
XX
PA   (CRIT-) CRITICAL THERAPEUTICS INC.
XX
PI   Newman W,  Qin S,  Okeefe T,  Obar R;
XX
DR   WPI; 2005-233483/24.
XX
PT   New antibody or its antigen-binding fragment specific to a vertebrate
PT   high mobility group box (HMGB) A box that inhibits release of a
PT   proinflammatory cytokine from a cell treated with HMGB protein, useful
PT   for treating, e.g. sepsis.
XX
PS   Disclosure; SEQ ID NO 2; 123pp; English.
XX
CC   The invention provides antibodies, or their antigen-binding fragments,
CC   that bind to a vertebrate high mobility group box (HMGB) polypeptide, to
CC   methods of detecting and/or identifying an agent that binds to an HMGB
CC   polypeptide, methods of treating a condition in a subject characterized
CC   by activation of an inflammatory cytokine cascade, and methods of
CC   detecting an HMGB polypeptide in a sample. The antibody (or antigen-
CC   binding fragment) binds to a vertebrate HMGB A box but does not
CC   specifically bind to non-A box epitopes of HMGB, and inhibits release of
CC   a proinflammatory cytokine from a vertebrate cell treated with an HMGB
CC   protein. A method of treating a condition characterized by activation of
CC   an inflammatory cytokine cascade comprises administering an antibody of
CC   the invention, or its antigen-binding fragment. The condition is selected
CC   from sepsis, allograft rejection, arthritis, asthma, lupus, adult
CC   respiratory distress syndrome, chronic obstructive pulmonary disease,
CC   psoriasis, pancreatitis, peritonitis, burns, ischemia, Behcet's disease,
CC   graft versus host disease, inflammatory bowel disease, multiple sclerosis
CC   and cachexia, especially sepsis, arthritis, or lupus. The present
CC   sequence is that of the A box of human HMGB1 ADY85012. An identical
CC   sequence is also found in rat and mouse HMGB1.
XX
SQ   Sequence 74 AA;

  Query Match             100.0%;  Score 110;  DB 9;  Length 74;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              ||||||||||||||||||||
Db          1 FKDPNAPKRLPSAFFLFCSE 20


RESULT 13
AAE35867
ID   AAE35867 standard; protein; 182 AA.
XX
AC   AAE35867;
XX
DT   17-JUN-2003  (first entry)
XX
DE   Human HMG1 protein mutant #1.
XX
KW   Human; high mobility group; HMG protein; HMG A box; HMG B box; asthma;
KW   inflammatory cytokine; endotoxic shock; rheumatoid arthritis; hepatitis;
KW   appendicitis; peptic ulcer; duodenal ulcer; Crohn's disease; meningitis;
KW   allergy; immune complex disease; sinusitis; bronchitis; atherosclerosis;
KW   emphysema; HIV infection; candidiasis; malaria; filariasis; myocarditis;
KW   Hodgkin's disease; neuritis; dermatitis; myocardial ischaemia; diabetes;
KW   Alzheimer's disease; Goodpasture's syndrome; graft-versus-host disease;
KW   amoebiasis; multiple sclerosis; gout; cerebral infarction; peritonitis;
KW   gene therapy; human immunodeficiency virus; HMGB1 protein; mutant;
KW   mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200292004-A2.
XX
PD   21-NOV-2002.
XX
PF   15-MAY-2002; 2002WO-US015329.
XX
PR   15-MAY-2001; 2001US-0291034P.
XX
PA   (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (UYPI-) UNIV PITTSBURGH.
XX
PI   Tracey KJ,  Yang H,  Warren HS,  Fink MP;
XX
DR   WPI; 2003-120594/11.
XX
PT   New isolated polypeptide having a vertebrate HMG A box, useful for
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PT   inhibiting a condition associated with an activated inflammatory cytokine
PT   cascade, e.g. endotoxic shock, myocardial infarction, asthma, HIV
PT   infection, malaria and diabetes.
XX
PS   Example 1; Page 37; 82pp; English.
XX
CC   The invention relates to high mobility group (HMG) protein comprising DNA
CC   binding motifs termed HMG A box and HMG B box. HMG A box or a non-
CC   naturally occurring HMG A box inhibits the release of a pro-inflammatory
CC   cytokine from a vertebrate cell. The methods and compositions of the
CC   invention are useful for inhibiting a condition characterised by
CC   activation of an inflammatory cytokine cascade such as endotoxic shock,
CC   rheumatoid arthritis, appendicitis, peptic or duodenal ulcers, Crohn's
CC   disease, peritonitis, hepatitis, asthma, allergy, immune complex disease,
CC   sinusitis, bronchitis, emphysema, HIV infection, candidiasis, malaria,
CC   filariasis, amoebiasis, dermatitis, atherosclerosis, Alzheimer's disease,
CC   myocarditis, myocardial ischaemia, meningitis, multiple sclerosis, gout,
CC   cerebral infarction, neuritis, Goodpasture's syndrome, graft-versus-host
CC   disease, diabetes and Hodgkin's disease. The invention is useful in gene
CC   therapy. The present sequence is human HMG1 (also termed as HMGB1)
CC   protein (carboxy terminus) mutant
XX
SQ   Sequence 182 AA;

  Query Match             100.0%;  Score 110;  DB 6;  Length 182;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              ||||||||||||||||||||
Db         89 FKDPNAPKRLPSAFFLFCSE 108


RESULT 14
ADO25936
ID   ADO25936 standard; protein; 182 AA.
XX
AC   ADO25936;
XX
DT   26-AUG-2004  (first entry)
XX
DE   Human high mobility group box 1 C-terminal mutant.
XX
KW   cytostatic; gene therapy; vaccine; pharmaceutical composition;
KW   HMGB B box; high mobility group; immune response; immunostimulation;
KW   cancer; human; high mobility group box 1; HMG1; cytokine activity;
KW   mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2004046338-A2.
XX
PD   03-JUN-2004.
XX
PF   19-NOV-2003; 2003WO-US036975.
XX
PR   20-NOV-2002; 2002US-0427848P.
XX
PA   (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
XX
PI   Tracey KJ;
XX
DR   WPI; 2004-420625/39.
XX
PT   New pharmaceutical composition comprises a polypeptide comprising an HMGB
PT   B box or its functional variant, useful for stimulating or increasing an
PT   immune response in an individual or for treating cancer in an individual.
XX
PS   Example 1; SEQ ID NO 19; 68pp; English.
XX
CC   The invention describes a pharmaceutical composition comprising a
CC   polypeptide comprising an HMGB (high mobility group box) B box or its
CC   functional variant to treat a disease or condition by increasing an
CC   immune response in an individual administered with the pharmaceutical
CC   composition. Also described are: an antibody attached to a polypeptide
CC   comprising an HMGB B box or its functional variant; stimulating or
CC   increasing an immune response in an individual in need of
CC   immunostimulation; and treating cancer in an individual. The composition
CC   is useful for stimulating or increasing an immune response in an
CC   individual in need of immunostimulation or for treating cancer in an
CC   individual. This is the amino acid sequence of a human high mobility
CC   group box 1 (HMG1) C-terminal mutant.
XX
SQ   Sequence 182 AA;

  Query Match             100.0%;  Score 110;  DB 8;  Length 182;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              ||||||||||||||||||||
Db         89 FKDPNAPKRLPSAFFLFCSE 108


RESULT 15
ADO71495
ID   ADO71495 standard; protein; 182 AA.
XX
AC   ADO71495;
XX
DT   26-AUG-2004  (first entry)
XX
DE   Human high mobility group box 1 (HMGB1) mutant protein #1.
XX
KW   Human; high mobility group box 1; HMGB1; HMGB; HMGB A box; HMGB B box;
KW   proinflammatory cytokine; weight loss; obesity; inflammation;
KW   inflammatory cytokine cascade; sepsis; allograft rejection;
KW   rheumatoid arthritis; asthma; lupus; adult respiratory distress syndrome;
KW   chronic obstructive pulmonary disease; psoriasis; pancreatitis;
KW   peritonitis; burn; myocardial ischaemia; organic ischaemia;
KW   reperfusion ischaemia; Behcet's disease; graft-versus-host disease;
KW   Crohn's disease; ulcerative colitis; multiple sclerosis; cachexia;
KW   mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2004046345-A2.
XX
PD   03-JUN-2004.
XX
PF   20-NOV-2003; 2003WO-US037507.
XX
PR   20-NOV-2002; 2002US-0427841P.
PR   20-NOV-2002; 2002US-0427846P.
XX
PA   (CRIT-) CRITICAL THERAPEUTICS INC.
XX
PI   Newman W,  O'keefe TL;
XX
DR   WPI; 2004-420628/39.
XX
PT   New high mobility group box proteins, useful in treating obesity, sepsis,
PT   rheumatoid arthritis, asthma, psoriasis, burns, myocardial ischemia,
PT   Behcet's disease, ulcerative colitis, multiple sclerosis, or cachexia.
XX
PS   Example 1; SEQ ID NO 19; 113pp; English.
XX
CC   The invention relates to a polypeptide comprising a high mobility group
CC   box protein (HMGB) A or B box. The HMGB A or B box can inhibit release of
CC   a proinflammatory cytokine from a cell treated with an HMGB protein. The
CC   invention also relates to a purified preparation of antibodies that
CC   specifically bind to the HMGB B box but do not specifically bind to non-B
CC   box epitopes of HMGB, where the antibodies can inhibit release of a
CC   proinflammatory cytokine from a cell treated with HMGB, a method for
```

CC effecting weight loss or treating obesity in a patient, a method of
CC determining whether a compound inhibits inflammation, a pharmaceutical
CC composition comprising an HMGB protein or an antibody that binds to the
CC protein, an agent that inhibits TNF biological activity and a method of
CC treating a condition in a patient characterised by activation of an
CC inflammatory cytokine cascade. Effecting weight loss or treating obesity
CC in a patient comprises administering to the patient an amount of the
CC polypeptide. The polypeptide, antibodies, composition and methods are
CC useful in treating obesity and conditions characterised by activation of
CC an inflammatory cytokine cascade, e.g. sepsis, allograft rejection,
CC rheumatoid arthritis, asthma, lupus, adult respiratory distress syndrome,
CC chronic obstructive pulmonary disease, psoriasis, pancreatitis,
CC peritonitis, burns, myocardial ischaemia, organic ischaemia, reperfusion
CC ischaemia, Behcet's disease, graft-versus-host disease, Crohn's disease,
CC ulcerative colitis, multiple sclerosis or cachexia. This sequence
CC represents a human HMGB1 mutant polypeptide of the invention.
XX
SQ Sequence 182 AA;

Query Match 100.0%; Score 110; DB 8; Length 182;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FKDPNAPKRLPSAFFLFCSE 20
||||||||||||||||||||
Db 89 FKDPNAPKRLPSAFFLFCSE 108

Search completed: April 6, 2006, 10:19:09
Job time : 25.2763 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 10:19:38 ; Search time 3.81579 Seconds
(without alignments)
504.309 Million cell updates/sec

Title: US-10-717-984-23
Perfect score: 110
Sequence: 1 FKDPNAPKRLPSAFFLFCSE 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	110	100.0	216	2	S29857	nonhistone chromos
2	103	93.6	170	2	A27853	nonhistone chromos
3	103	93.6	215	1	NSRTH1	nonhistone chromos
4	103	93.6	215	1	S01947	nonhistone chromos
5	103	93.6	215	2	S02826	nonhistone chromos
6	103	93.6	215	2	A28897	nonhistone chromos
7	103	93.6	215	2	I48688	non-histone chromo
8	100	90.9	210	2	S62355	high mobility grou
9	97	88.2	186	2	S30221	nonhistone chromos
10	97	88.2	207	2	JC1129	nonhistone chromos
11	97	88.2	207	2	JC1114	high-mobility grou
12	97	88.2	209	1	NSHUH2	nonhistone chromos
13	97	88.2	210	2	A34719	nonhistone chromos
14	97	88.2	210	2	S54774	high mobility grou
15	95	86.4	49	2	D61510	high mobility grou
16	93	84.5	201	2	I50254	HMG-1 - chicken
17	93	84.5	202	2	S22359	nonhistone chromos
18	91	82.7	215	2	I51067	gene HMG-T2 protei
19	89	80.9	205	2	S26062	nonhistone chromos
20	87	79.1	172	2	A24019	nonhistone chromos
21	87	79.1	204	2	S48708	high-mobility-grou
22	87	79.1	204	2	T01071	high mobility grou
23	84	76.4	186	2	B61611	nonhistone chromos
24	79	71.8	141	2	T09581	probable high mobi
25	77	70.0	157	2	B47150	high mobility grou
26	77	70.0	161	2	S18991	high mobility grou
27	77	70.0	168	2	T03640	high mobility grou
28	76	69.1	393	2	JC6179	dorsal switch prot
29	76	69.1	393	2	S50068	nonhistone chromos
30	75	68.2	126	2	T03375	high mobility grou
31	75	68.2	141	2	T07377	high mobility grou
32	75	68.2	142	2	T02252	high mobility grou
33	75	68.2	152	2	S22309	high mobility grou
34	74	67.3	178	2	T51159	HMG protein [impor
35	73	66.4	149	2	S39556	high mobility grou
36	72	65.5	138	2	F84553	probable HMG prote
37	72	65.5	138	2	T51596	high mobility grou
38	72	65.5	144	2	S40302	high mobility grou
39	72	65.5	154	2	S40122	high mobility grou
40	67	60.9	95	2	T43006	HMG protein 1.1 -
41	67	60.9	312	2	T27004	hypothetical prote
42	66	60.0	200	2	JC4357	HMG1 protein - sea
43	64	58.2	93	2	A35072	nonhistone chromos
44	64	58.2	125	2	T04662	high mobility grou
45	64	58.2	141	2	T51598	high mobility grou

ALIGNMENTS

RESULT 1
S29857
nonhistone chromosomal protein HMG-1 - human
C;Species: Homo sapiens (man)
C;Date: 08-Dec-1993 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C;Accession: S29857
R;Stros, M.; Dixon, G.H.
Biochim. Biophys. Acta 1172, 231-235, 1993
A;Title: A retropseudogene for non-histone chromosomal protein HMG-1.
A;Reference number: S29857; MUID:93176821; PMID:8439568
A;Accession: S29857
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-216 <STR>
A;Cross-references: UNIPARC:UPI000011DFAA; EMBL:L08048; NID:g184250; PIDN:AAA64970.1; PII
A;Note: the authors did not translate the codon for residue 1
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

Query Match 100.0%; Score 110; DB 2; Length 216;
Best Local Similarity 100.0%; Pred. No. 6.5e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FKDPNAPKRLPSAFFLFCSE 20
||||||||||||||||||||
Db 89 FKDPNAPKRLPSAFFLFCSE 108

RESULT 2
A27853
nonhistone chromosomal protein HMG-1 - Chinese hamster (fragment)
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: A27853
R;Lee, K.L.D.; Pentecost, B.T.; D'Anna, J.A.; Tobey, R.A.; Gurley, L.R.; Dixon, G.H.
Nucleic Acids Res. 15, 5051-5068, 1987
A;Title: Characterization of cDNA sequences corresponding to three distinct HMG-1 mRNA sp
A;Reference number: A27853; MUID:87259986; PMID:3601666
A;Accession: A27853
A;Molecule type: mRNA
A;Residues: 1-170 <LEE>
A;Cross-references: UNIPROT:P07156; UNIPARC:UPI00001771D5
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;1-38/Domain: HMG box homology (fragment) <HMG1>
F;47-121/Domain: HMG box homology <HMG2>

Query Match 93.6%; Score 103; DB 2; Length 170;
Best Local Similarity 95.0%; Pred. No. 6.6e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              |||||||||  ||||||||||
Db         44 FKDPNAPKRPPSAFFLFCSE 63
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RESULT 3
NSRTH1
nonhistone chromosomal protein HMG-1 - rat
N;Alternate names: 30K heparin-binding protein, brain; amphoterin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A41175; A27298; A30188; B48771; A48771; C48771
R;Merenmies, J.; Pihlaskari, R.; Laitinen, J.; Wartiovaara, J.; Rauvala, H.
J. Biol. Chem. 266, 16722-16729, 1991
A;Title: 30-kDa heparin-binding protein of brain (amphoterin) involved in neurite outgrc
A;Reference number: A41175; MUID:91358468; PMID:1885601
A;Accession: A41175
A;Molecule type: mRNA
A;Residues: 1-215 <MER>
A;Cross-references: UNIPROT:P07155; UNIPARC:UPI00000008A6; GB:M64986; NID:g202884; PIDN:
A;Note: part of this sequence, including the amino end of the mature protein, was confir
A;Note: the authors used antibodies to synthetic peptides to demonstrate this protein in
h-mobility group proteins
R;Paonessa, G.; Frank, R.; Cortese, R.
Nucleic Acids Res. 15, 9077, 1987
A;Title: Nucleotide sequence of rat liver HMG1 cDNA.
A;Reference number: A27298; MUID:88067717; PMID:3684582
A;Accession: A27298
A;Molecule type: mRNA
A;Residues: 1-10,'R',12-82,84-95,97,'AS',100-215 <PAO>
A;Cross-references: UNIPARC:UPI0000173984
R;Rauvala, H.; Merenmies, J.; Pihlaskari, R.; Korkolainen, M.; Huhtala, M.L.; Panula, P.
J. Cell Biol. 107, 2293-2305, 1988
A;Title: The adhesive and neurite-promoting molecule p30: analysis of the amino-terminal
 brain neurons.
A;Reference number: A30188; MUID:89066894; PMID:2461949
A;Accession: A30188
A;Molecule type: protein
A;Residues: 2-14,'X',16-21 <RAU>
A;Cross-references: UNIPARC:UPI0000173985
R;Parkkinen, J.; Raulo, E.; Merenmies, J.; Nolo, R.; Kajander, E.O.; Baumann, M.; Rauval
J. Biol. Chem. 268, 19726-19738, 1993
A;Title: Amphoterin, the 30-kDa protein in a family of HMG1-type polypeptides. Enhanced
A;Reference number: A48771; MUID:93374971; PMID:8366113
A;Accession: B48771
A;Status: preliminary
A;Molecule type: protein
A;Residues: 98-105,'X',107-112 <PA2>
A;Cross-references: UNIPARC:UPI0000173986
A;Experimental source: postnatal brain
A;Note: sequence extracted from NCBI backbone (NCBIP:137788)
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;2-215/Product: nonhistone chromosomal protein HMG-1 #status experimental <MAT>
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

  Query Match   93.6%; Score 103; DB 1; Length 215;
  Best Local Similarity   95.0%; Pred. No. 8.3e-09;
  Matches   19; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

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Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              |||||||||  ||||||||||
Db         89 FKDPNAPKRPPSAFFLFCSE 108
```

RESULT 4
S01947
nonhistone chromosomal protein HMG-1 - bovine
N;Alternate names: 33K protein; high-mobility-group protein HMG-1
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1989 #sequence_revision 22-Apr-1995 #text_change 09-Jul-2004
C;Accession: S01947; A61611; S10959; I45910
R;Kaplan, D.J.; Duncan, C.H.
Nucleic Acids Res. 16, 10375, 1988
A;Title: Full length cDNA sequence for bovine high mobility group 1 (HMG1) protein.
A;Reference number: S01947; MUID:89057489; PMID:3194213
A;Accession: S01947
A;Molecule type: mRNA
A;Residues: 1-215 <KAP>
A;Cross-references: UNIPROT:P10103; UNIPARC:UPI000016C31D; EMBL:X12796; NID:g416; PIDN:CA
R;Walker, J.M.; Gooderham, K.; Hastings, J.R.B.; Mayes, E.; Johns, E.W.
FEBS Lett. 122, 264-270, 1980
A;Title: The primary structures of non-histone chromosomal proteins HMG 1 and 2.
A;Reference number: A61611; MUID:81138848; PMID:7202717
A;Accession: A61611
A;Molecule type: protein
A;Residues: 2-22,'S',24-40;48-105,'A',107-157,'X',160-193,'D',195 <WAL>
A;Cross-references: UNIPARC:UPI0000173987; UNIPARC:UPI0000173988
R;Christen, T.; Bischoff, M.; Hobi, R.; Kuenzle, C.C.
FEBS Lett. 267, 139-141, 1990
A;Title: High mobility group proteins 1 and 2 bind preferentially to brominated poly(dG-c
A;Reference number: S10726; MUID:90306387; PMID:2365081
A;Accession: S10959
A;Molecule type: protein
A;Residues: 2-22,'X',24-38 <CHR>
A;Cross-references: UNIPARC:UPI0000173989
R;Pentecost, B.T.; Dixon, G.H.
Biosci. Rep. 4, 49-57, 1984
A;Title: Isolation and partial sequence of bovine cDNA clones for the high-mobility-group
A;Reference number: I45910; MUID:84128872; PMID:6141822
A;Accession: I45910
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 'PGG',119,'V',121-215 <PEN>
A;Cross-references: UNIPARC:UPI000016C31E; GB:M26110; NID:g163156; PIDN:AAA30567.1; PID:g
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; duplication; nucleus
F;2-215/Product: nonhistone chromosomal protein HMG-1 #status predicted <MAT>
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

  Query Match   93.6%; Score 103; DB 1; Length 215;
  Best Local Similarity   95.0%; Pred. No. 8.3e-09;
  Matches   19; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

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Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              |||||||||  ||||||||||
Db         89 FKDPNAPKRPPSAFFLFCSE 108
```

RESULT 5
S02826
nonhistone chromosomal protein HMG-1 - human
C;Species: Homo sapiens (man)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C;Accession: S02826; A33178; G33178
R;Wen, L.; Huang, J.K.; Johnson, B.H.; Reeck, G.R.
Nucleic Acids Res. 17, 1197-1214, 1989
A;Title: A human placental cDNA clone that encodes nonhistone chromosomal protein HMG-1.
A;Reference number: S02826; MUID:89160247; PMID:2922262
A;Accession: S02826
A;Molecule type: mRNA
A;Residues: 1-215 <WEN>
A;Cross-references: UNIPROT:P09429; UNIPARC:UPI00000015ED; EMBL:X12597; NID:g32326; PIDN
R;Ward, L.D.; Hong, J.; Whitehead, R.H.; Simpson, R.J.
Electrophoresis 11, 883-891, 1990
A;Title: Development of a database of amino acid sequences for human colon carcinoma prot
A;Reference number: A33178; MUID:91176935; PMID:2079031
A;Accession: A33178
A;Molecule type: protein
A;Residues: 2-13,'XXF' <WAR>
A;Cross-references: UNIPARC:UPI00001771D7
A;Accession: G33178
A;Molecule type: protein

```
A;Residues: 2-13,'XX',16-22 <WA2>
A;Cross-references: UNIPARC:UPI00001771D7
C;Genetics:
A;Gene: GDB:HMG1
A;Cross-references: GDB:133789; OMIM:163905
A;Map position: 13q12-13q12
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

  Query Match             93.6%;  Score 103;  DB 2;  Length 215;
  Best Local Similarity   95.0%;  Pred. No. 8.3e-09;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              |||||||||  ||||||||||
Db         89 FKDPNAPKRPPSAFFLFCSE 108


RESULT 6
A28897
nonhistone chromosomal protein HMG-1 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: A28897
R;Tsuda, K.; Kikuchi, M.; Mori, K.; Waga, S.; Yoshida, M.
Biochemistry 27, 6159-6163, 1988
A;Title: Primary structure of non-histone protein HMG1 revealed by the nucleotide sequen
A;Reference number: A28897; MUID:89050965; PMID:3191113
A;Accession: A28897
A;Molecule type: mRNA
A;Residues: 1-215 <TSU>
A;Cross-references: UNIPROT:P12682; UNIPARC:UPI000016C6C4; GB:M21683; GB:M21684; NID:g16
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

  Query Match             93.6%;  Score 103;  DB 2;  Length 215;
  Best Local Similarity   95.0%;  Pred. No. 8.3e-09;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              |||||||||  ||||||||||
Db         89 FKDPNAPKRPPSAFFLFCSE 108


RESULT 7
I48688
non-histone chromosomal high-mobility group 1 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48688; A55402; I57021
R;Yotov, W.V.; St-Arnaud, R.
Nucleic Acids Res. 20, 3516, 1992
A;Title: Nucleotide sequence of a mouse cDNA encoding the nonhistone chromosomal high mo
A;Reference number: I48687; MUID:92335012; PMID:1630928
A;Accession: I48688
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-215 <RES>
A;Cross-references: UNIPROT:P07155; UNIPARC:UPI00000008A6; EMBL:Z11997; NID:g53381; PIDN
R;Ferrari, S.; Ronfani, L.; Calogero, S.; Bianchi, M.E.
J. Biol. Chem. 269, 28803-28808, 1994
A;Title: The mouse gene coding for high mobility group 1 protein (HMG1).
A;Reference number: A55402; MUID:95050689; PMID:7961836
A;Accession: A55402
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-189,'E',191-215 <FER>
A;Cross-references: UNIPARC:UPI000016CDD6; EMBL:X80457; NID:g620097; PIDN:CAA56631.1; PI
R;Pauken, C.M.; Nagle, D.L.; Bucan, M.; Lo, C.W.
Mamm. Genome 5, 91-99, 1994
A;Title: Molecular cloning, expression analysis, and chromosomal localization of mouse Hm
A;Reference number: I57021; MUID:94235965; PMID:8180479
A;Accession: I57021
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-215 <RE2>
A;Cross-references: UNIPARC:UPI00000008A6; EMBL:U00431; NID:g437101; PIDN:AAA20508.1; PI
C;Genetics:
A;Gene: hmg1
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

  Query Match             93.6%;  Score 103;  DB 2;  Length 215;
  Best Local Similarity   95.0%;  Pred. No. 8.3e-09;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              |||||||||  ||||||||||
Db         89 FKDPNAPKRPPSAFFLFCSE 108


RESULT 8
S62355
high mobility group protein 1 - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S62355
R;Nightingale, K.; Dimitrov, S.; Reeves, R.; Wolffe, A.P.
EMBO J. 15, 548-561, 1996
A;Title: Evidence for a shared structural role for HMG1 and linker histones B4 and H1 in
A;Reference number: S62355; MUID:96174815; PMID:8599938
A;Accession: S62355
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-210 <NIG>
A;Cross-references: UNIPROT:Q91596; UNIPARC:UPI00000FB3E3; EMBL:U21933; NID:g709958; PIDN
A;Note: the authors did not translate the codon for residue 1
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
F;6-82/Domain: HMG box homology <HMG1>
F;91-165/Domain: HMG box homology <HMG2>

  Query Match             90.9%;  Score 100;  DB 2;  Length 210;
  Best Local Similarity   90.0%;  Pred. No. 2.4e-08;
  Matches   18;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              |||||||||  |||||||||:
Db         88 FKDPNAPKRPPSAFFLFCSD 107


RESULT 9
S30221
nonhistone chromosomal protein HMG-2B - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: S30221
R;Alexandre, S.; Li, W.W.; Lee, A.S.
Nucleic Acids Res. 20, 6413, 1992
A;Title: A human HMG2 cDNA with a novel 3'-untranslated region.
A;Reference number: S30221; MUID:93117123; PMID:1475204
A;Accession: S30221
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-186 <ALE>
A;Cross-references: UNIPROT:P26583; UNIPARC:UPI000016AA6C; EMBL:Z17240; NID:g32334; PIDN
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1992
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein
F;1-60/Domain: HMG box homology (fragment) <HMG>
F;69-143/Domain: HMG box homology <HMG1>
```

```
  Query Match             88.2%;  Score 97;  DB 2;  Length 186;
  Best Local Similarity   94.7%;  Pred. No. 6.4e-08;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 KDPNAPKRLPSAFFLFCSE 20
              |||||||| ||||||||||
Db         67 KDPNAPKRPPSAFFLFCSE 85


RESULT 10
JC1129
nonhistone chromosomal protein HMG-2 - chicken
N;Alternate names: high-mobility-group protein 2
C;Species: Gallus gallus (chicken)
C;Date: 05-Mar-1993 #sequence_revision 05-Mar-1993 #text_change 09-Jul-2004
C;Accession: JC1129
R;Sparrow, D.B.; Wells, J.R.E.
Gene 114, 289-290, 1992
A;Title: Sequence of a cDNA encoding chicken high-mobility-group protein-2.
A;Reference number: JC1129; MUID:92290291; PMID:1601311
A;Accession: JC1129
A;Molecule type: mRNA
A;Residues: 1-207 <SPA>
A;Cross-references: UNIPROT:P26584; UNIPARC:UPI0000171348; GB:M80574; NID:g211928; PIDN:
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

  Query Match             88.2%;  Score 97;  DB 2;  Length 207;
  Best Local Similarity   94.7%;  Pred. No. 7.1e-08;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 KDPNAPKRLPSAFFLFCSE 20
              |||||||| ||||||||||
Db         90 KDPNAPKRPPSAFFLFCSE 108


RESULT 11
JC1114
high-mobility group protein 2 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004
C;Accession: JC1114
R;Davis, D.L.; Burch, J.B.E.
Gene 113, 251-256, 1992
A;Title: Isolation of a chicken HMG2 cDNA clone and evidence for an HMG2-specific 3'-unt
A;Reference number: JC1114; MUID:92241676; PMID:1572546
A;Accession: JC1114
A;Molecule type: mRNA
A;Residues: 1-207 <DAV>
A;Cross-references: UNIPROT:P26584; UNIPARC:UPI0000171347; GB:M83235; NID:g211926; PIDN:
C;Comment: The high mobility group proteins are among the most abundant nonhistone chrom
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

  Query Match             88.2%;  Score 97;  DB 2;  Length 207;
  Best Local Similarity   94.7%;  Pred. No. 7.1e-08;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 KDPNAPKRLPSAFFLFCSE 20
              |||||||| ||||||||||
Db         90 KDPNAPKRPPSAFFLFCSE 108


RESULT 12
NSHUH2
nonhistone chromosomal protein HMG-2 - human
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: A42425; S20061; S18068
R;Shirakawa, H.; Yoshida, M.
J. Biol. Chem. 267, 6641-6645, 1992
A;Title: Structure of a gene coding for human HMG2 protein.
A;Reference number: A42425; MUID:92202209; PMID:1551873
A;Accession: A42425
A;Molecule type: DNA
A;Residues: 2-209 <SHI>
A;Cross-references: UNIPROT:P26583; UNIPARC:UPI000012CA25; GB:M83665; NID:g184235; PIDN:
A;Note: sequence extracted from NCBI backbone (NCBIN:89899, NCBIP:89900)
A;Note: initiator Met not shown
R;Majumdar, A.; Brown, D.; Kerby, S.; Rudzinski, I.; Polte, T.; Randhawa, Z.; Seidman, M
Nucleic Acids Res. 19, 6643, 1991
A;Title: Sequence of human HMG2 cDNA.
A;Reference number: S20061; MUID:92093633; PMID:1754403
A;Accession: S20061
A;Molecule type: mRNA
A;Residues: 1-209 <MAJ>
A;Cross-references: UNIPARC:UPI000013E34D; EMBL:X62534; NID:g32332; PIDN:CAA44395.1; PID
C;Genetics:
A;Gene: GDB:NHCP2
A;Cross-references: GDB:119451; OMIM:118880
A;Map position: 7pter-7qter
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

  Query Match             88.2%;  Score 97;  DB 1;  Length 209;
  Best Local Similarity   94.7%;  Pred. No. 7.2e-08;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 KDPNAPKRLPSAFFLFCSE 20
              |||||||| ||||||||||
Db         90 KDPNAPKRPPSAFFLFCSE 108


RESULT 13
A34719
nonhistone chromosomal protein HMG-2 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 09-Jul-2004
C;Accession: A34719
R;Shirakawa, H.; Tsuda, K.; Yoshida, M.
Biochemistry 29, 4419-4423, 1990
A;Title: Primary structure of non-histone chromosomal protein HMG2 revealed by the nuclec
A;Reference number: A34719; MUID:90275208; PMID:2350545
A;Accession: A34719
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-210 <SHI>
A;Cross-references: UNIPROT:P17741; UNIPARC:UPI000016C6C5; GB:J02895; NID:g164491; PIDN:
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
C;Keywords: chromosomal protein; DNA binding; nucleus
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

  Query Match             88.2%;  Score 97;  DB 2;  Length 210;
  Best Local Similarity   94.7%;  Pred. No. 7.2e-08;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 KDPNAPKRLPSAFFLFCSE 20
              |||||||| ||||||||||
Db         90 KDPNAPKRPPSAFFLFCSE 108


RESULT 14
S54774
high mobility group 2 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S54774; S52211
R;Zwilling, S.; Koenig, H.; Wirth, T.
```

EMBO J. 14, 1198-1208, 1995
A;Title: High mobility group protein 2 functionally interacts with the POU domains of oc
A;Reference number: S54774; MUID:95237201; PMID:7720710
A;Accession: S54774
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-210 <ZWI>
A;Cross-references: UNIPROT:P30681; UNIPARC:UPI000016432C; EMBL:Z46757; NID:g609168; PID
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology
F;6-83/Domain: HMG box homology <HMG1>
F;92-166/Domain: HMG box homology <HMG2>

  Query Match 88.2%; Score 97; DB 2; Length 210;
  Best Local Similarity 94.7%; Pred. No. 7.2e-08;
  Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          2 KDPNAPKRLPSAFFLFCSE 20
              |||||||| ||||||||||
Db         90 KDPNAPKRPPSAFFLFCSE 108
```

RESULT 15
D61510
high mobility group protein 1 - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: D61510
R;Grossberger, D.; Flajnik, M.; Marcuz, A.
Comp. Biochem. Physiol. B 98, 127-133, 1991
A;Title: Ribosomal and chromosomal protein cDNA clones of Xenopus laevis thymus isolated
A;Reference number: A61510; MUID:91284580; PMID:2060276
A;Accession: D61510
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-49 <GRO>
A;Cross-references: UNIPROT:Q7LZL5; UNIPARC:UPI00001771D3
C;Superfamily: nonhistone chromosomal protein HMG-2; HMG box homology

  Query Match 86.4%; Score 95; DB 2; Length 49;
  Best Local Similarity 89.5%; Pred. No. 3.5e-08;
  Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          2 KDPNAPKRLPSAFFLFCSE 20
              |||||||| |||||:||||
Db          7 KDPNAPKRPPSAFFIFCSE 25
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Search completed: April 6, 2006, 10:26:17
Job time : 3.81579 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 10:13:48 ; Search time 23.6184 Seconds
(without alignments)
597.439 Million cell updates/sec

Title: US-10-717-984-23
Perfect score: 110
Sequence: 1 FKDPNAPKRLPSAFFLFCSE 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	110	100.0	215	2	Q8BQ02_MOUSE	Q8bq02 mus musculu
2	104	94.5	208	2	Q80YZ1_MOUSE	Q80yz1 mus musculu
3	104	94.5	216	2	Q90228_AMBME	Q90228 ambystoma m
4	103	93.6	132	2	Q5T7C1_HUMAN	Q5t7c1 homo sapien
5	103	93.6	157	2	Q5T7C2_HUMAN	Q5t7c2 homo sapien
6	103	93.6	158	2	Q5T7C4_HUMAN	Q5t7c4 homo sapien
7	103	93.6	162	2	Q5T7C6_HUMAN	Q5t7c6 homo sapien
8	103	93.6	176	2	Q59GW1_HUMAN	Q59gw1 homo sapien
9	103	93.6	178	2	Q8C7C4_MOUSE	Q8c7c4 mus musculu
10	103	93.6	180	1	HMG1_CRIGR	P07156 cricetulus
11	103	93.6	181	2	Q8BNM0_MOUSE	Q8bnm0 mus musculu
12	103	93.6	192	2	Q5T7C5_HUMAN	Q5t7c5 homo sapien
13	103	93.6	206	2	Q5BKQ1_MOUSE	Q5bkq1 mus musculu
14	103	93.6	211	2	Q9NQJ4_HUMAN	Q9nqj4 homo sapien
15	103	93.6	211	2	Q6P4N5_XENTR	Q6p4n5 xenopus tro
16	103	93.6	211	2	Q7SZ42_XENLA	Q7sz42 xenopus lae
17	103	93.6	214	1	HMG1_BOVIN	P10103 bos taurus
18	103	93.6	214	1	HMG1_CANFA	Q6yka4 canis famil
19	103	93.6	214	1	HMG1_HUMAN	P09429 homo sapien
20	103	93.6	214	1	HMG1_MOUSE	P63158 mus musculu
21	103	93.6	214	1	HMG1_PIG	P12682 sus scrofa
22	103	93.6	214	1	HMG1_RAT	P63159 rattus norv
23	103	93.6	214	2	Q9PUK9_CHICK	Q9puk9 gallus gall
24	103	93.6	215	2	Q14321_HUMAN	Q14321 homo sapien
25	103	93.6	215	2	Q5T7C3_HUMAN	Q5t7c3 homo sapien
26	103	93.6	215	2	Q4R844_MACFA	Q4r844 macaca fasc
27	103	93.6	215	2	O88611_SPAEH	O88611 spalax leuc
28	103	93.6	215	2	O88612_SPAEH	O88612 spalax leuc
29	103	93.6	215	2	Q9QWY6_SPAEH	Q9qwy6 spalax leuc
30	103	93.6	215	2	Q9QX40_SPAEH	Q9qx40 spalax leuc
31	103	93.6	215	2	Q548R9_RAT	Q548r9 rattus norv
32	103	93.6	215	2	Q58EV5_MOUSE	Q58ev5 m high mobi
33	103	93.6	215	2	Q9YH06_CHICK	Q9yh06 gallus gall
34	101	91.8	205	2	Q6NX86_BRARE	Q6nx86 brachydanio
35	101	91.8	205	2	Q7ZVC6_BRARE	Q7zvc6 brachydanio
36	100	90.9	199	2	Q4RRH9_TETNG	Q4rrh9 tetraodon n
37	100	90.9	210	2	Q91596_XENLA	Q91596 xenopus lae
38	100	90.9	210	2	Q6GNQ5_XENLA	Q6gnq5 xenopus lae
39	100	90.9	211	1	HMG1X_HUMAN	Q9ugv6 homo sapien
40	97	88.2	190	2	Q9CT19_MOUSE	Q9ct19 mus musculu
41	97	88.2	195	2	Q96J53_HUMAN	Q96j53 homo sapien
42	97	88.2	200	2	Q6Y235_PAGMA	Q6y235 pagrus majo
43	97	88.2	201	1	HMG4_CHICK	P40618 gallus gall
44	97	88.2	206	1	HMG2_CHICK	P26584 gallus gall
45	97	88.2	208	1	HMG2_HUMAN	P26583 homo sapien

ALIGNMENTS

RESULT 1
Q8BQ02_MOUSE
ID Q8BQ02_MOUSE PRELIMINARY; PRT; 215 AA.
AC Q8BQ02;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length
DE enriched library, clone:D130095O09 product:high mobility group box 1,
DE full insert sequence.
GN Name=Hmgb1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";

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RL   Nature 420:563-573(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK051800; BAC34773.1; -; mRNA.
DR   HSSP; P07155; 1CKT.
DR   SMR; Q8BQ02; 2-84, 93-171.
DR   MGI; MGI:96113; Hmgb1.
DR   GO; GO:0005615; C:extracellular space; IDA.
DR   GO; GO:0005634; C:nucleus; TAS.
DR   GO; GO:0030235; F:nitric-oxide synthase regulator activity; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0006809; P:nitric oxide biosynthesis; IDA.
DR   GO; GO:0006810; P:transport; IDA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
SQ   SEQUENCE   215 AA;  24905 MW;  8A86969266DC07F5 CRC64;

  Query Match             100.0%;  Score 110;  DB 2;  Length 215;
  Best Local Similarity   100.0%;  Pred. No. 2e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              ||||||||||||||||||||
Db         89 FKDPNAPKRLPSAFFLFCSE 108


RESULT 2
Q80YZ1_MOUSE
ID   Q80YZ1_MOUSE PRELIMINARY;      PRT;   208 AA.
AC   Q80YZ1;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   BM168F16.1 (Novel protein similar to high-mobility group box 1
DE   (Hmgb1)).
GN   Name=bM168F16.1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   North P., Leaves N., Greystrong J., Coppola M., Manjunath S.,
RA   Russell E., Smith M., Strachan G., Tofts C., Boal E., Cobley V.,
RA   Hunter G., Kimberley C., Thomas D., Cave-Berry L., Weston P.,
RA   Botcherby M.R.M.;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL670999; CAD83017.1; -; Genomic_DNA.
DR   HSSP; P07156; 1NHN.
DR   SMR; Q80YZ1; 2-84, 93-171.
DR   Ensembl; ENSMUSG00000064154; Mus musculus.
DR   GO; GO:0000785; C:chromatin; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
SQ   SEQUENCE   208 AA;  23811 MW;  4DBCB7B9516D7B52 CRC64;

  Query Match             94.5%;  Score 104;  DB 2;  Length 208;
  Best Local Similarity   95.0%;  Pred. No. 1.8e-08;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              ||||||||| ||||||||||
Db         89 FKDPNAPKRSPSAFFLFCSE 108


RESULT 3
Q90228_AMBME
ID   Q90228_AMBME PRELIMINARY;      PRT;   216 AA.
AC   Q90228;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   High mobility group protein-2 (HMG-2).
GN   Name=HMG-2;
OS   Ambystoma mexicanum (Axolotl).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
OC   Ambystoma.
OX   NCBI_TaxID=8296;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RX   MEDLINE=96263706; PubMed=8654668; DOI=10.1016/0145-305X(95)00025-O;
RA   de Guerra A., Guillet F., Charlemagne J., Fellah J.S.;
RT   "Identification of cDNA clones encoding HMG 2, a major protein of the
RT   mexican axolotl hydrocortisone-sensitive thymocytes.";
RL   Dev. Comp. Immunol. 19:417-423(1995).
RN   [2]
RP   PROTEIN SEQUENCE.
RX   PubMed=2097001;
RA   Guillet F., Tournefier A., Denoulet P., Capony J.P., Kerfourn F.,
RA   Charlemagne J.;
RT   "High levels of HMG1-2 protein expression in the cytoplasm and nucleus
RT   of hydrocortisone sensitive amphibian thymocytes.";
RL   Biol. Cell 69:153-160(1990).
DR   EMBL; U31513; AAB08831.1; -; mRNA.
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DR   PIR; A60975; A60975.
DR   HSSP; P07155; 1CKT.
DR   SMR; Q90228; 2-84, 90-167.
DR   GO; GO:0000785; C:chromatin; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
SQ   SEQUENCE   216 AA;  24703 MW;  E6E096F85B4EA5C4 CRC64;

  Query Match             94.5%;  Score 104;  DB 2;  Length 216;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-08;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 KDPNAPKRLPSAFFLFCSE 20
              ||||||||||||||||||||
Db         91 KDPNAPKRLPSAFFLFCSE 109


RESULT 4
Q5T7C1_HUMAN
ID   Q5T7C1_HUMAN PRELIMINARY;      PRT;   132 AA.
AC   Q5T7C1;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   High-mobility group box 1 (Fragment).
GN   Name=HMGB1; ORFNames=RP11-550P23.1-006;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Pelan S.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL353648; CAI15605.1; -; Genomic_DNA.
DR   SMR; Q5T7C1; 2-84.
DR   GO; GO:0000785; C:chromatin; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
FT   NON_TER     132    132
SQ   SEQUENCE   132 AA;  15185 MW;  C0FAC527E53F9356 CRC64;

  Query Match             93.6%;  Score 103;  DB 2;  Length 132;
  Best Local Similarity   95.0%;  Pred. No. 1.7e-08;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              ||||||||| ||||||||||
Db         89 FKDPNAPKRPPSAFFLFCSE 108


RESULT 5
Q5T7C2_HUMAN
ID   Q5T7C2_HUMAN PRELIMINARY;      PRT;   157 AA.
AC   Q5T7C2;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   High-mobility group box 1 (Fragment).
GN   Name=HMGB1; ORFNames=RP11-550P23.1-009;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Pelan S.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL353648; CAI15604.1; -; Genomic_DNA.
DR   SMR; Q5T7C2; 2-84, 89-157.
DR   GO; GO:0000785; C:chromatin; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
FT   NON_TER     157    157
SQ   SEQUENCE   157 AA;  18164 MW;  F38343E7F52FC457 CRC64;

  Query Match             93.6%;  Score 103;  DB 2;  Length 157;
  Best Local Similarity   95.0%;  Pred. No. 2e-08;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              ||||||||| ||||||||||
Db         89 FKDPNAPKRPPSAFFLFCSE 108


RESULT 6
Q5T7C4_HUMAN
ID   Q5T7C4_HUMAN PRELIMINARY;      PRT;   158 AA.
AC   Q5T7C4;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   High-mobility group box 1.
GN   Name=HMGB1; ORFNames=RP11-550P23.1-003;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Pelan S.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL353648; CAI15603.1; -; Genomic_DNA.
DR   SMR; Q5T7C4; 2-84, 89-157.
DR   GO; GO:0000785; C:chromatin; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
SQ   SEQUENCE   158 AA;  18311 MW;  1A438343E7F52FC4 CRC64;

  Query Match             93.6%;  Score 103;  DB 2;  Length 158;
  Best Local Similarity   95.0%;  Pred. No. 2e-08;
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  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              ||||||||| ||||||||||
Db         89 FKDPNAPKRPPSAFFLFCSE 108


RESULT 7
Q5T7C6_HUMAN
ID   Q5T7C6_HUMAN PRELIMINARY;      PRT;   162 AA.
AC   Q5T7C6;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   High-mobility group box 1 (Fragment).
GN   Name=HMGB1; ORFNames=RP11-550P23.1-002;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Pelan S.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL353648; CAI15601.1; -; Genomic_DNA.
DR   SMR; Q5T7C6; 2-84, 89-144.
DR   GO; GO:0000785; C:chromatin; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
FT   NON_TER     162    162
SQ   SEQUENCE   162 AA;  18808 MW;  4866095637D6FA88 CRC64;

  Query Match             93.6%;  Score 103;  DB 2;  Length 162;
  Best Local Similarity   95.0%;  Pred. No. 2.1e-08;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              ||||||||| ||||||||||
Db         89 FKDPNAPKRPPSAFFLFCSE 108


RESULT 8
Q59GW1_HUMAN
ID   Q59GW1_HUMAN PRELIMINARY;      PRT;   176 AA.
AC   Q59GW1;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   High-mobility group box 1 variant (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Myeloblast cell line;
RA   Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RA   Ohara O., Nagase T., Kikuno F.R.;
RT   "None Title.";
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB208998; BAD92235.1; -; mRNA.
FT   NON_TER     1      1
SQ   SEQUENCE   176 AA;  20164 MW;  C31A7039D92649D9 CRC64;

  Query Match             93.6%;  Score 103;  DB 2;  Length 176;
  Best Local Similarity   95.0%;  Pred. No. 2.2e-08;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              ||||||||| ||||||||||
Db         91 FKDPNAPKRPPSAFFLFCSE 110


RESULT 9
Q8C7C4_MOUSE
ID   Q8C7C4_MOUSE PRELIMINARY;      PRT;   178 AA.
AC   Q8C7C4;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-
DE   length enriched library, clone:C920030E14 product:high mobility group
DE   box 1, full insert sequence. (Fragment).
GN   Name=Hmgb1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
```

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RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK050659; BAC34367.1; -; mRNA.
DR   HSSP; P07156; 1NHN.
DR   SMR; Q8C7C4; 2-84, 93-171.
DR   MGI; MGI:96113; Hmgb1.
DR   GO; GO:0005615; C:extracellular space; IDA.
DR   GO; GO:0005634; C:nucleus; TAS.
DR   GO; GO:0030235; F:nitric-oxide synthase regulator activity; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0006809; P:nitric oxide biosynthesis; IDA.
DR   GO; GO:0006810; P:transport; IDA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
FT   NON_TER     178    178
SQ   SEQUENCE   178 AA;  20303 MW;  155FD80D52960A62 CRC64;

  Query Match             93.6%;  Score 103;  DB 2;  Length 178;
  Best Local Similarity   95.0%;  Pred. No. 2.3e-08;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              |||||||||  ||||||||||
Db         89 FKDPNAPKRPPSAFFLFCSE 108


RESULT 10
HMG1_CRIGR
ID   HMG1_CRIGR     STANDARD;      PRT;   180 AA.
AC   P07156;
DT   01-APR-1988 (Rel. 07, Created)
DT   01-APR-1988 (Rel. 07, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   High mobility group protein 1 (HMG-1) (High mobility group protein B1)
DE   (Fragment).
GN   Name=HMGB1; Synonyms=HMG-1, HMG1;
OS   Cricetulus griseus (Chinese hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Cricetidae; Cricetinae; Cricetulus.
OX   NCBI_TaxID=10029;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX   MEDLINE=87259986; PubMed=3601666;
RA   Lee K.-L.D., Pentecost B.T., D'Anna J.A., Tobey R.A., Gurley L.R.,
RA   Dixon G.H.;
RT   "Characterization of cDNA sequences corresponding to three distinct
RT   HMG-1 mRNA species in line CHO Chinese hamster cells and cell cycle
RT   expression of the HMG-1 gene.";
RL   Nucleic Acids Res. 15:5051-5068(1987).
RN   [2]
RP   STRUCTURE BY NMR OF 57-136.
RX   MEDLINE=93347974; PubMed=8346022;
RA   Read C.M., Cary P.D., Crane-Robinson C., Driscoll P.C., Norman D.G.;
RT   "Solution structure of a DNA-binding domain from HMG1.";
RL   Nucleic Acids Res. 21:3427-3436(1993).
CC   -!- FUNCTION: Binds preferentially single-stranded DNA and unwinds
CC       double stranded DNA.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- SIMILARITY: Belongs to the HMG1/HMG2 protein family.
CC   -!- SIMILARITY: Contains 2 HMG box DNA-binding domains.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; Y00365; CAA68441.1; -; Genomic_DNA.
DR   PIR; A27853; A27853.
DR   PDB; 1HSM; NMR; @=58-136.
DR   PDB; 1HSN; NMR; @=58-136.
DR   PDB; 1NHM; NMR; @=58-136.
DR   PDB; 1NHN; NMR; @=58-136.
DR   SMR; P07156; 1-49.
DR   GO; GO:0000793; C:condensed chromosome; ISS.
DR   GO; GO:0008301; F:DNA bending activity; ISS.
DR   GO; GO:0005515; F:protein binding; ISS.
DR   GO; GO:0006288; P:base-excision repair, DNA ligation; ISS.
DR   GO; GO:0006310; P:DNA recombination; ISS.
DR   GO; GO:0006281; P:DNA repair; ISS.
DR   GO; GO:0006268; P:DNA unwinding; ISS.
DR   GO; GO:0006325; P:establishment and/or maintenance of chromat. . .; ISS.
DR   GO; GO:0017055; P:negative regulation of transcriptional prei. . .; ISS.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
KW   3D-structure; Chromosomal protein; DNA-binding; Nuclear protein;
KW   Repeat.
FT   DNA_BIND     <1     44       HMG box 1.
FT   DNA_BIND     60    128       HMG box 2.
FT   COMPBIAS    151    180       Asp/Glu-rich (acidic).
FT   NON_TER       1      1
FT   HELIX        67     81
FT   TURN         83     84
FT   TURN         87     88
FT   HELIX        89     97
FT   TURN         98    100
FT   HELIX       103    128
SQ   SEQUENCE   180 AA;  20904 MW;  F624392F41609854 CRC64;

  Query Match             93.6%;  Score 103;  DB 1;  Length 180;
  Best Local Similarity   95.0%;  Pred. No. 2.3e-08;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              |||||||||  ||||||||||
Db         54 FKDPNAPKRPPSAFFLFCSE 73
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RESULT 11
Q8BNM0_MOUSE
ID   Q8BNM0_MOUSE PRELIMINARY;      PRT;   181 AA.
AC   Q8BNM0;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mus musculus 7 days embryo whole body cDNA, RIKEN full-length enriched
DE   library, clone:C430013M12 product:high mobility group box 1, full
DE   insert sequence. (Fragment).
GN   Name=Hmgb1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK082902; BAC38678.1; -; mRNA.
DR   HSSP; P07156; 1NHN.
DR   SMR; Q8BNM0; 2-84, 93-171.
DR   MGI; MGI:96113; Hmgb1.
DR   GO; GO:0005615; C:extracellular space; IDA.
DR   GO; GO:0005634; C:nucleus; TAS.
DR   GO; GO:0030235; F:nitric-oxide synthase regulator activity; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0006809; P:nitric oxide biosynthesis; IDA.
DR   GO; GO:0006810; P:transport; IDA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
FT   NON_TER     181    181
SQ   SEQUENCE   181 AA;  20648 MW;  B31D82055FD80D52 CRC64;

  Query Match             93.6%;  Score 103;  DB 2;  Length 181;
  Best Local Similarity   95.0%;  Pred. No. 2.3e-08;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              |||||||||| ||||||||||
Db         89 FKDPNAPKRPPSAFFLFCSE 108


RESULT 12
Q5T7C5_HUMAN
ID   Q5T7C5_HUMAN PRELIMINARY;      PRT;   192 AA.
AC   Q5T7C5;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   High-mobility group box 1 (Fragment).
GN   Name=HMGB1; ORFNames=RP11-550P23.1-001;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Pelan S.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL353648; CAI15602.1; -; Genomic_DNA.
DR   SMR; Q5T7C5; 2-84, 93-171.
DR   GO; GO:0000785; C:chromatin; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
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DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
FT   NON_TER     192    192
SQ   SEQUENCE   192 AA;  22050 MW;  6A52DB61DA307C1D CRC64;

  Query Match             93.6%;  Score 103;  DB 2;  Length 192;
  Best Local Similarity   95.0%;  Pred. No. 2.5e-08;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              |||||||||  ||||||||||
Db         89 FKDPNAPKRPPSAFFLFCSE 108


RESULT 13
Q5BKQ1_MOUSE
ID   Q5BKQ1_MOUSE PRELIMINARY;      PRT;   206 AA.
AC   Q5BKQ1;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Testis;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Testis;
RA   Director MGC Project;
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC090989; AAH90989.1; -; mRNA.
DR   InterPro; IPR010486; HdeA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   InterPro; IPR012287; Homeodomain-rel.
DR   InterPro; IPR011993; PH_type.
DR   InterPro; IPR011991; Wing_hlx_DNA_bd.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   206 AA;  23569 MW;  3F06A32D1A618B98 CRC64;

  Query Match             93.6%;  Score 103;  DB 2;  Length 206;
  Best Local Similarity   95.0%;  Pred. No. 2.7e-08;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              |||||||||  ||||||||||
Db         89 FKDPNAPKRPPSAFFLFCSE 108


RESULT 14
Q9NQJ4_HUMAN
ID   Q9NQJ4_HUMAN PRELIMINARY;      PRT;   211 AA.
AC   Q9NQJ4;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   OTTHUMP00000031372.
GN   Name=HMG1L1; ORFNames=RP4-579F20.2-001;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Howden P.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL160176; CAB92731.1; -; Genomic_DNA.
DR   HSSP; P07155; 1HMF.
DR   SMR; Q9NQJ4; 2-84, 93-171.
DR   Ensembl; ENSG00000124097; Homo sapiens.
DR   HGNC; HGNC:4993; HMG1L1.
DR   GO; GO:0000785; C:chromatin; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
SQ   SEQUENCE   211 AA;  24238 MW;  D2623FDE00FA8355 CRC64;

  Query Match             93.6%;  Score 103;  DB 2;  Length 211;
  Best Local Similarity   95.0%;  Pred. No. 2.7e-08;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              |||||||||  ||||||||||
Db         89 FKDPNAPKRPPSAFFLFCSE 108


RESULT 15
Q6P4N5_XENTR
ID   Q6P4N5_XENTR PRELIMINARY;      PRT;   211 AA.
AC   Q6P4N5;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein MGC75695.
GN   Name=MGC75695;
OS   Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Silurana.
OX   NCBI_TaxID=8364;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
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RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RA   Klein S., Gerhard D.S.;
RL   Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC063332; AAH63332.1; -; mRNA.
DR   HSSP; P07155; 1AAB.
DR   SMR; Q6P4N5; 2-84, 89-165.
DR   GO; GO:0000785; C:chromatin; IEA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000135; Highmoblty_12.
DR   InterPro; IPR000910; HMG_12_box.
DR   Pfam; PF00505; HMG_box; 2.
DR   PRINTS; PR00886; HIGHMOBLTY12.
DR   SMART; SM00398; HMG; 2.
DR   PROSITE; PS00353; HMG_BOX_1; 1.
DR   PROSITE; PS50118; HMG_BOX_2; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   211 AA;  24479 MW;  C32185AD038D9FA3 CRC64;

  Query Match             93.6%;  Score 103;  DB 2;  Length 211;
  Best Local Similarity   95.0%;  Pred. No. 2.7e-08;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              |||||||||  ||||||||||
Db         89 FKDPNAPKRPPSAFFLFCSE 108


Search completed: April  6, 2006, 10:25:15
Job time : 26.6184 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 10:25:39 ; Search time 5.72368 Seconds
(without alignments)
288.890 Million cell updates/sec

Title: US-10-717-984-23
Perfect score: 110
Sequence: 1 FKDPNAPKRLPSAFFLFCSE 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	103	93.6	214	2	US-09-538-092-883	Sequence 883, App
2	103	93.6	214	2	US-09-214-881A-1	Sequence 1, Appli
3	103	93.6	214	2	US-09-214-881A-3	Sequence 3, Appli
4	103	93.6	214	2	US-09-214-881A-4	Sequence 4, Appli
5	103	93.6	214	2	US-09-214-881A-5	Sequence 5, Appli
6	100	90.9	213	2	US-09-949-016-10813	Sequence 10813, A
7	97	88.2	206	2	US-09-214-881A-9	Sequence 9, Appli
8	97	88.2	208	2	US-09-538-092-1018	Sequence 1018, Ap
9	97	88.2	208	2	US-09-214-881A-2	Sequence 2, Appli
10	97	88.2	209	2	US-09-214-881A-6	Sequence 6, Appli
11	97	88.2	209	2	US-09-214-881A-8	Sequence 8, Appli
12	97	88.2	320	2	US-09-949-016-10728	Sequence 10728, A
13	97	88.2	879	2	US-09-914-259-38	Sequence 38, Appl
14	96	87.3	59	2	US-09-513-999C-4826	Sequence 4826, Ap
15	96	87.3	110	2	US-09-513-999C-4824	Sequence 4824, Ap
16	96	87.3	110	2	US-09-513-999C-4825	Sequence 4825, Ap
17	93	84.5	122	2	US-09-513-999C-4966	Sequence 4966, Ap
18	93	84.5	200	2	US-09-702-705-324	Sequence 324, App
19	93	84.5	200	2	US-09-702-705-789	Sequence 789, App
20	93	84.5	200	2	US-09-736-457-324	Sequence 324, App
21	93	84.5	200	2	US-09-736-457-789	Sequence 789, App
22	93	84.5	200	2	US-09-614-124B-324	Sequence 324, App
23	93	84.5	200	2	US-09-614-124B-789	Sequence 789, App
24	93	84.5	200	2	US-09-671-325-324	Sequence 324, App
25	93	84.5	200	2	US-09-671-325-789	Sequence 789, App
26	93	84.5	200	2	US-09-589-184-324	Sequence 324, App
27	93	84.5	200	2	US-09-589-184-789	Sequence 789, App
28	93	84.5	200	2	US-09-658-824-324	Sequence 324, App
29	93	84.5	200	2	US-09-658-824-789	Sequence 789, App
30	93	84.5	200	2	US-10-017-754-324	Sequence 324, App
31	93	84.5	200	2	US-10-017-754-789	Sequence 789, App
32	93	84.5	200	2	US-09-651-563-324	Sequence 324, App
33	93	84.5	200	2	US-09-651-563-789	Sequence 789, App
34	93	84.5	200	2	US-09-519-642-324	Sequence 324, App
35	93	84.5	200	2	US-09-519-642-789	Sequence 789, App
36	93	84.5	201	2	US-09-214-881A-10	Sequence 10, Appl
37	93	84.5	207	2	US-09-702-705-1667	Sequence 1667, Ap
38	93	84.5	207	2	US-09-736-457-1667	Sequence 1667, Ap
39	93	84.5	207	2	US-09-614-124B-1667	Sequence 1667, Ap
40	93	84.5	207	2	US-09-671-325-1667	Sequence 1667, Ap
41	93	84.5	207	2	US-09-658-824-1667	Sequence 1667, Ap
42	93	84.5	207	2	US-10-017-754-1667	Sequence 1667, Ap
43	93	84.5	207	2	US-10-017-754-1913	Sequence 1913, Ap
44	93	84.5	207	2	US-09-651-563-1667	Sequence 1667, Ap
45	93	84.5	228	2	US-09-949-016-10496	Sequence 10496, A

ALIGNMENTS

RESULT 1
US-09-538-092-883
; Sequence 883, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 883
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P09429
US-09-538-092-883

Query Match 93.6%; Score 103; DB 2; Length 214;
Best Local Similarity 95.0%; Pred. No. 5.2e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FKDPNAPKRLPSAFFLFCSE 20
||||||||| ||||||||||
Db 88 FKDPNAPKRPPSAFFLFCSE 107

RESULT 2
US-09-214-881A-1
; Sequence 1, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
; APPLICANT: Uesugi, Hiroko
; APPLICANT: Okazaki, Takahiro
; APPLICANT: Tanaka, Masao
; APPLICANT: Nakao, Kazuwa
; APPLICANT: Yoshida, Michiteru
; APPLICANT: Shirakawa, Hitoshi
; APPLICANT: Osakada, Fumio

; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-214-881A-1

Query Match 93.6%; Score 103; DB 2; Length 214;
Best Local Similarity 95.0%; Pred. No. 5.2e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FKDPNAPKRLPSAFFLFCSE 20
||||||||| ||||||||||
Db 88 FKDPNAPKRPPSAFFLFCSE 107

RESULT 3
US-09-214-881A-3
; Sequence 3, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
; APPLICANT: Uesugi, Hiroko
; APPLICANT: Okazaki, Takahiro
; APPLICANT: Tanaka, Masao
; APPLICANT: Nakao, Kazuwa
; APPLICANT: Yoshida, Michiteru
; APPLICANT: Shirakawa, Hitoshi
; APPLICANT: Osakada, Fumio
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-214-881A-3

Query Match 93.6%; Score 103; DB 2; Length 214;
Best Local Similarity 95.0%; Pred. No. 5.2e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FKDPNAPKRLPSAFFLFCSE 20
||||||||| ||||||||||
Db 88 FKDPNAPKRPPSAFFLFCSE 107

RESULT 4
US-09-214-881A-4
; Sequence 4, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
; APPLICANT: Uesugi, Hiroko
; APPLICANT: Okazaki, Takahiro
; APPLICANT: Tanaka, Masao
; APPLICANT: Nakao, Kazuwa
; APPLICANT: Yoshida, Michiteru
; APPLICANT: Shirakawa, Hitoshi
; APPLICANT: Osakada, Fumio
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-214-881A-4

Query Match 93.6%; Score 103; DB 2; Length 214;
Best Local Similarity 95.0%; Pred. No. 5.2e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FKDPNAPKRLPSAFFLFCSE 20
||||||||| ||||||||||
Db 88 FKDPNAPKRPPSAFFLFCSE 107

RESULT 5
US-09-214-881A-5
; Sequence 5, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
; APPLICANT: Uesugi, Hiroko
; APPLICANT: Okazaki, Takahiro
; APPLICANT: Tanaka, Masao
; APPLICANT: Nakao, Kazuwa
; APPLICANT: Yoshida, Michiteru
; APPLICANT: Shirakawa, Hitoshi
; APPLICANT: Osakada, Fumio
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Rattus rattus
US-09-214-881A-5

Query Match 93.6%; Score 103; DB 2; Length 214;
Best Local Similarity 95.0%; Pred. No. 5.2e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FKDPNAPKRLPSAFFLFCSE 20
||||||||| ||||||||||
Db 88 FKDPNAPKRPPSAFFLFCSE 107

RESULT 6
US-09-949-016-10813
; Sequence 10813, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10813

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;   LENGTH: 213
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-10813

  Query Match             90.9%;  Score 100;  DB 2;  Length 213;
  Best Local Similarity   94.7%;  Pred. No. 1.6e-08;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCS 19
              ||||||||| |||||||||
Db         91 FKDPNAPKRTPSAFFLFCS 109


RESULT 7
US-09-214-881A-9
; Sequence 9, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
;  APPLICANT:  Ozaki, Shoichi
;  APPLICANT:  Sobajima, Junko
;  APPLICANT:  Uesugi, Hiroko
;  APPLICANT:  Okazaki, Takahiro
;  APPLICANT:  Tanaka, Masao
;  APPLICANT:  Nakao, Kazuwa
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION:  DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE:  068383.0104
;  CURRENT APPLICATION NUMBER: US/09/214,881A
;  CURRENT FILING DATE:  1999-06-07
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 206
;   TYPE: PRT
;   ORGANISM: Gallus gallus
US-09-214-881A-9

  Query Match             88.2%;  Score 97;  DB 2;  Length 206;
  Best Local Similarity   94.7%;  Pred. No. 4.8e-08;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 KDPNAPKRLPSAFFLFCSE 20
              |||||||| ||||||||||
Db         89 KDPNAPKRPPSAFFLFCSE 107


RESULT 8
US-09-538-092-1018
; Sequence 1018, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
;  APPLICANT: Giot, Loic
;  APPLICANT:  Mansfield, Traci A.
;  TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
;  FILE REFERENCE: 15966-542
;  CURRENT APPLICATION NUMBER: US/09/538,092
;  CURRENT FILING DATE:  2000-03-29
;  PRIOR APPLICATION NUMBER: 60/127,352
;  PRIOR FILING DATE: 1999-04-01
;  PRIOR APPLICATION NUMBER: 60/178,965
;  PRIOR FILING DATE: 2000-02-01
;  NUMBER OF SEQ ID NOS: 1387
;  SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1018
;   LENGTH: 208
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Polypeptide Accession Number P26583
US-09-538-092-1018

  Query Match             88.2%;  Score 97;  DB 2;  Length 208;
  Best Local Similarity   94.7%;  Pred. No. 4.8e-08;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 KDPNAPKRLPSAFFLFCSE 20
              |||||||| ||||||||||
Db         89 KDPNAPKRPPSAFFLFCSE 107


RESULT 9
US-09-214-881A-2
; Sequence 2, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
;  APPLICANT:  Ozaki, Shoichi
;  APPLICANT:  Sobajima, Junko
;  APPLICANT:  Uesugi, Hiroko
;  APPLICANT:  Okazaki, Takahiro
;  APPLICANT:  Tanaka, Masao
;  APPLICANT:  Nakao, Kazuwa
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION:  DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE:  068383.0104
;  CURRENT APPLICATION NUMBER: US/09/214,881A
;  CURRENT FILING DATE:  1999-06-07
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 208
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-214-881A-2

  Query Match             88.2%;  Score 97;  DB 2;  Length 208;
  Best Local Similarity   94.7%;  Pred. No. 4.8e-08;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 KDPNAPKRLPSAFFLFCSE 20
              |||||||| ||||||||||
Db         89 KDPNAPKRPPSAFFLFCSE 107


RESULT 10
US-09-214-881A-6
; Sequence 6, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
;  APPLICANT:  Ozaki, Shoichi
;  APPLICANT:  Sobajima, Junko
;  APPLICANT:  Uesugi, Hiroko
;  APPLICANT:  Okazaki, Takahiro
;  APPLICANT:  Tanaka, Masao
;  APPLICANT:  Nakao, Kazuwa
;  APPLICANT:  Yoshida, Michiteru
;  APPLICANT:  Shirakawa, Hitoshi
;  APPLICANT:  Osakada, Fumio
;  TITLE OF INVENTION:  DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
;  FILE REFERENCE:  068383.0104
;  CURRENT APPLICATION NUMBER: US/09/214,881A
;  CURRENT FILING DATE:  1999-06-07
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 209
;   TYPE: PRT
;   ORGANISM: Sus scrofa
US-09-214-881A-6
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Query Match 88.2%; Score 97; DB 2; Length 209;
Best Local Similarity 94.7%; Pred. No. 4.8e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          2 KDPNAPKRLPSAFFLFCSE 20
              |||||||| ||||||||||
Db         89 KDPNAPKRPPSAFFLFCSE 107
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RESULT 11
US-09-214-881A-8
; Sequence 8, Application US/09214881A
; Patent No. 6822078
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Shoichi
; APPLICANT: Sobajima, Junko
; APPLICANT: Uesugi, Hiroko
; APPLICANT: Okazaki, Takahiro
; APPLICANT: Tanaka, Masao
; APPLICANT: Nakao, Kazuwa
; APPLICANT: Yoshida, Michiteru
; APPLICANT: Shirakawa, Hitoshi
; APPLICANT: Osakada, Fumio
; TITLE OF INVENTION: DIAGNOSTIC DRUGS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 068383.0104
; CURRENT APPLICATION NUMBER: US/09/214,881A
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Rattus rattus
US-09-214-881A-8

Query Match 88.2%; Score 97; DB 2; Length 209;
Best Local Similarity 94.7%; Pred. No. 4.8e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          2 KDPNAPKRLPSAFFLFCSE 20
              |||||||| ||||||||||
Db         89 KDPNAPKRPPSAFFLFCSE 107
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RESULT 12
US-09-949-016-10728
; Sequence 10728, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10728
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10728

Query Match 88.2%; Score 97; DB 2; Length 320;
Best Local Similarity 94.7%; Pred. No. 7.7e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          2 KDPNAPKRLPSAFFLFCSE 20
              |||||||| ||||||||||
Db        201 KDPNAPKRPPSAFFLFCSE 219
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RESULT 13
US-09-914-259-38
; Sequence 38, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 879
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-914-259-38

Query Match 88.2%; Score 97; DB 2; Length 879;
Best Local Similarity 90.0%; Pred. No. 2.3e-07;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 FKDPNAPKRLPSAFFLFCSE 20
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Db        763 FKDPNAPKRPPLAFFLFCSE 782
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RESULT 14
US-09-513-999C-4826
; Sequence 4826, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4826
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-4826

Query Match 87.3%; Score 96; DB 2; Length 59;
Best Local Similarity 90.0%; Pred. No. 1.8e-08;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              || |||||| ||||||||||
Db         38 FKGPNAPKRPPSAFFLFCSE 57
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RESULT 15
US-09-513-999C-4824
; Sequence 4824, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.

; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4824
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 91
; OTHER INFORMATION: Xaa=Asp or Gly
US-09-513-999C-4824

Query Match 87.3%; Score 96; DB 2; Length 110;
Best Local Similarity 90.0%; Pred. No. 3.5e-08;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              || |||||| ||||||||||
Db         89 FKXPNAPKRPPSAFFLFCSE 108
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OM protein - protein search, using sw model

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(without alignments)
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Title: US-10-717-984-23
Perfect score: 110
Sequence: 1 FKDPNAPKRLPSAFFLFCSE 20

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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	110	100.0	20	4	US-10-147-447-16	Sequence 16, Appl
2	110	100.0	20	4	US-10-300-072-23	Sequence 23, Appl
3	110	100.0	20	4	US-10-456-949-16	Sequence 16, Appl
4	110	100.0	20	4	US-10-456-947-45	Sequence 45, Appl
5	110	100.0	20	4	US-10-718-495-23	Sequence 23, Appl
6	110	100.0	20	4	US-10-717-984-23	Sequence 23, Appl
7	110	100.0	74	4	US-10-147-447-20	Sequence 20, Appl
8	110	100.0	74	4	US-10-300-072-20	Sequence 20, Appl
9	110	100.0	74	4	US-10-300-072-53	Sequence 53, Appl
10	110	100.0	74	4	US-10-456-949-20	Sequence 20, Appl
11	110	100.0	74	4	US-10-456-947-8	Sequence 8, Appli
12	110	100.0	74	4	US-10-456-947-39	Sequence 39, Appl
13	110	100.0	74	4	US-10-718-495-20	Sequence 20, Appl
14	110	100.0	74	4	US-10-718-495-53	Sequence 53, Appl
15	110	100.0	74	4	US-10-717-984-20	Sequence 20, Appl
16	110	100.0	74	4	US-10-717-984-53	Sequence 53, Appl
17	110	100.0	74	5	US-10-938-992-3	Sequence 3, Appli
18	110	100.0	74	5	US-10-938-992-69	Sequence 69, Appl
19	110	100.0	182	4	US-10-147-447-19	Sequence 19, Appl
20	110	100.0	182	4	US-10-300-072-19	Sequence 19, Appl
21	110	100.0	182	4	US-10-456-949-19	Sequence 19, Appl
22	110	100.0	182	4	US-10-718-495-19	Sequence 19, Appl
23	110	100.0	182	4	US-10-717-984-19	Sequence 19, Appl
24	110	100.0	216	4	US-10-147-447-18	Sequence 18, Appl
25	110	100.0	216	4	US-10-300-072-18	Sequence 18, Appl
26	110	100.0	216	4	US-10-300-072-24	Sequence 24, Appl
27	110	100.0	216	4	US-10-456-949-18	Sequence 18, Appl
28	110	100.0	216	4	US-10-456-947-6	Sequence 6, Appli
29	110	100.0	216	4	US-10-456-947-10	Sequence 10, Appl
30	110	100.0	216	4	US-10-718-495-18	Sequence 18, Appl
31	110	100.0	216	4	US-10-718-495-24	Sequence 24, Appl
32	110	100.0	216	4	US-10-717-984-18	Sequence 18, Appl
33	110	100.0	216	4	US-10-717-984-24	Sequence 24, Appl
34	110	100.0	216	5	US-10-938-992-1	Sequence 1, Appli
35	103	93.6	74	4	US-10-300-072-51	Sequence 51, Appl
36	103	93.6	74	4	US-10-300-072-54	Sequence 54, Appl
37	103	93.6	74	4	US-10-300-072-56	Sequence 56, Appl
38	103	93.6	74	4	US-10-456-947-37	Sequence 37, Appl
39	103	93.6	74	4	US-10-456-947-40	Sequence 40, Appl
40	103	93.6	74	4	US-10-456-947-42	Sequence 42, Appl
41	103	93.6	74	4	US-10-718-495-51	Sequence 51, Appl
42	103	93.6	74	4	US-10-718-495-54	Sequence 54, Appl
43	103	93.6	74	4	US-10-718-495-56	Sequence 56, Appl
44	103	93.6	74	4	US-10-717-984-51	Sequence 51, Appl
45	103	93.6	74	4	US-10-717-984-54	Sequence 54, Appl

ALIGNMENTS

RESULT 1
US-10-147-447-16
; Sequence 16, Application US/10147447
; Publication No. US20030060410A1
; GENERAL INFORMATION:
; APPLICANT: Tracey, Kevin J.
; APPLICANT: Yang, Huan
; APPLICANT: Warren Jr., Howland Shaw
; APPLICANT: Fink, Mitchell P.
; TITLE OF INVENTION: Use of HMG Fragments as
; TITLE OF INVENTION: Anti-Inflammatory Agents
; FILE REFERENCE: 3268.1001-001
; CURRENT APPLICATION NUMBER: US/10/147,447
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/291,034
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-147-447-16

Query Match 100.0%; Score 110; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FKDPNAPKRLPSAFFLFCSE 20
||||||||||||||||||||
Db 1 FKDPNAPKRLPSAFFLFCSE 20

RESULT 2
US-10-300-072-23
; Sequence 23, Application US/10300072
; Publication No. US20030144201A1
; GENERAL INFORMATION:
; APPLICANT: Kevin J. Tracey
; APPLICANT: Huan Yang
; APPLICANT: Howland Shaw Warren, Jr.
; APPLICANT: Mitchell P. Fink
; TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS ANTI-FLAMMATORY
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 3268.1001-005
; CURRENT APPLICATION NUMBER: US/10/300,072
; CURRENT FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: US 10/147,447
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/291,034

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;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-300-072-23

  Query Match            100.0%;  Score 110;  DB 4;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 2.4e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              ||||||||||||||||||||
Db          1 FKDPNAPKRLPSAFFLFCSE 20


RESULT 3
US-10-456-949-16
; Sequence 16, Application US/10456949
; Publication No. US20040005316A1
; GENERAL INFORMATION:
;  APPLICANT: Kevin J. Tracey
;  APPLICANT:  Huan Yang
;  TITLE OF INVENTION: USE OF HMG FRAGMENTS AS
;  TITLE OF INVENTION:  ANTI-INFLAMMATORY AGENTS
;  FILE REFERENCE: 3268.1001-006
;  CURRENT APPLICATION NUMBER: US/10/456,949
;  CURRENT FILING DATE:  2003-06-06
;  PRIOR APPLICATION NUMBER: 10/147,447
;  PRIOR FILING DATE: 2002-05-15
;  PRIOR APPLICATION NUMBER: 60/291,034
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-456-949-16

  Query Match            100.0%;  Score 110;  DB 4;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 2.4e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              ||||||||||||||||||||
Db          1 FKDPNAPKRLPSAFFLFCSE 20


RESULT 4
US-10-456-947-45
; Sequence 45, Application US/10456947
; Publication No. US20040053841A1
; GENERAL INFORMATION:
;  APPLICANT: Kevin J. Tracey
;  APPLICANT:  Huan Yang
;  TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN
;  TITLE OF INVENTION:  HMGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS
;  TITLE OF INVENTION:  ANTI-INFLAMMATORY AGENTS
;  FILE REFERENCE: 3268.1001-007
;  CURRENT APPLICATION NUMBER: US/10/456,947
;  CURRENT FILING DATE:  2003-06-06
;  PRIOR APPLICATION NUMBER: 10/147,447
;  PRIOR FILING DATE: 2002-05-15
;  PRIOR APPLICATION NUMBER: 60/291,034
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-456-947-45

  Query Match            100.0%;  Score 110;  DB 4;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 2.4e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              ||||||||||||||||||||
Db          1 FKDPNAPKRLPSAFFLFCSE 20


RESULT 5
US-10-718-495-23
; Sequence 23, Application US/10718495
; Publication No. US20040141948A1
; GENERAL INFORMATION:
;  APPLICANT: O'Keefe, Theresa L.
;  TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS
;  TITLE OF INVENTION:  ANTI-INFLAMMATORY AGENTS
;  FILE REFERENCE: 3258.1009-001
;  CURRENT APPLICATION NUMBER: US/10/718,495
;  CURRENT FILING DATE:  2003-11-12
;  PRIOR APPLICATION NUMBER: 60/427,841
;  PRIOR FILING DATE: 2002-11-20
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-718-495-23

  Query Match            100.0%;  Score 110;  DB 4;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 2.4e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              ||||||||||||||||||||
Db          1 FKDPNAPKRLPSAFFLFCSE 20


RESULT 6
US-10-717-984-23
; Sequence 23, Application US/10717984
; Publication No. US20040156851A1
; GENERAL INFORMATION:
;  APPLICANT: Newman, Walter
;  TITLE OF INVENTION: HMGB1 COMBINATION THERAPIES
;  FILE REFERENCE: 3258.1008-001
;  CURRENT APPLICATION NUMBER: US/10/717,984
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,846
;  PRIOR FILING DATE: 2002-11-20
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-717-984-23

  Query Match            100.0%;  Score 110;  DB 4;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 2.4e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              ||||||||||||||||||||
Db          1 FKDPNAPKRLPSAFFLFCSE 20


RESULT 7
US-10-147-447-20
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; Sequence 20, Application US/10147447
; Publication No. US20030060410A1
; GENERAL INFORMATION:
; APPLICANT: Tracey, Kevin J.
; APPLICANT: Yang, Huan
; APPLICANT: Warren Jr., Howland Shaw
; APPLICANT: Fink, Mitchell P.
; TITLE OF INVENTION: Use of HMG Fragments as
; TITLE OF INVENTION: Anti-Inflammatory Agents
; FILE REFERENCE: 3268.1001-001
; CURRENT APPLICATION NUMBER: US/10/147,447
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/291,034
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-147-447-20

Query Match 100.0%; Score 110; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 9.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FKDPNAPKRLPSAFFLFCSE 20
||||||||||||||||||||
Db 1 FKDPNAPKRLPSAFFLFCSE 20

RESULT 8
US-10-300-072-20
; Sequence 20, Application US/10300072
; Publication No. US20030144201A1
; GENERAL INFORMATION:
; APPLICANT: Kevin J. Tracey
; APPLICANT: Huan Yang
; APPLICANT: Howland Shaw Warren, Jr.
; APPLICANT: Mitchell P. Fink
; TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS ANTI-FLAMMATORY
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 3268.1001-005
; CURRENT APPLICATION NUMBER: US/10/300,072
; CURRENT FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: US 10/147,447
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/291,034
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-300-072-20

Query Match 100.0%; Score 110; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 9.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FKDPNAPKRLPSAFFLFCSE 20
||||||||||||||||||||
Db 1 FKDPNAPKRLPSAFFLFCSE 20

RESULT 9
US-10-300-072-53
; Sequence 53, Application US/10300072
; Publication No. US20030144201A1
; GENERAL INFORMATION:
; APPLICANT: Kevin J. Tracey
; APPLICANT: Huan Yang
; APPLICANT: Howland Shaw Warren, Jr.
; APPLICANT: Mitchell P. Fink
; TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS ANTI-FLAMMATORY
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 3268.1001-005
; CURRENT APPLICATION NUMBER: US/10/300,072
; CURRENT FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: US 10/147,447
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/291,034
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-300-072-53

Query Match 100.0%; Score 110; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 9.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FKDPNAPKRLPSAFFLFCSE 20
||||||||||||||||||||
Db 1 FKDPNAPKRLPSAFFLFCSE 20

RESULT 10
US-10-456-949-20
; Sequence 20, Application US/10456949
; Publication No. US20040005316A1
; GENERAL INFORMATION:
; APPLICANT: Kevin J. Tracey
; APPLICANT: Huan Yang
; TITLE OF INVENTION: USE OF HMG FRAGMENTS AS
; TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS
; FILE REFERENCE: 3268.1001-006
; CURRENT APPLICATION NUMBER: US/10/456,949
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 10/147,447
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/291,034
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-456-949-20

Query Match 100.0%; Score 110; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 9.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FKDPNAPKRLPSAFFLFCSE 20
||||||||||||||||||||
Db 1 FKDPNAPKRLPSAFFLFCSE 20

RESULT 11
US-10-456-947-8
; Sequence 8, Application US/10456947
; Publication No. US20040053841A1
; GENERAL INFORMATION:
; APPLICANT: Kevin J. Tracey
; APPLICANT: Huan Yang
; TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN
; TITLE OF INVENTION: HMGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS
; TITLE OF INVENTION: ANTI-INFLAMMATORY AGENTS
; FILE REFERENCE: 3268.1001-007
; CURRENT APPLICATION NUMBER: US/10/456,947

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;  CURRENT FILING DATE:  2003-06-06
;  PRIOR APPLICATION NUMBER: 10/147,447
;  PRIOR FILING DATE: 2002-05-15
;  PRIOR APPLICATION NUMBER: 60/291,034
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 74
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-456-947-8

  Query Match             100.0%;  Score 110;  DB 4;  Length 74;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              ||||||||||||||||||||
Db          1 FKDPNAPKRLPSAFFLFCSE 20


RESULT 12
US-10-456-947-39
; Sequence 39, Application US/10456947
; Publication No. US20040053841A1
; GENERAL INFORMATION:
;  APPLICANT: Kevin J. Tracey
;  APPLICANT:  Huan Yang
;  TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN
;  TITLE OF INVENTION:  HMGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS
;  TITLE OF INVENTION:  ANTI-INFLAMMATORY AGENTS
;  FILE REFERENCE: 3268.1001-007
;  CURRENT APPLICATION NUMBER: US/10/456,947
;  CURRENT FILING DATE:  2003-06-06
;  PRIOR APPLICATION NUMBER: 10/147,447
;  PRIOR FILING DATE: 2002-05-15
;  PRIOR APPLICATION NUMBER: 60/291,034
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39
;   LENGTH: 74
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-456-947-39

  Query Match             100.0%;  Score 110;  DB 4;  Length 74;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              ||||||||||||||||||||
Db          1 FKDPNAPKRLPSAFFLFCSE 20


RESULT 13
US-10-718-495-20
; Sequence 20, Application US/10718495
; Publication No. US20040141948A1
; GENERAL INFORMATION:
;  APPLICANT: O'Keefe, Theresa L.
;  TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS
;  TITLE OF INVENTION:  ANTI-INFLAMMATORY AGENTS
;  FILE REFERENCE: 3258.1009-001
;  CURRENT APPLICATION NUMBER: US/10/718,495
;  CURRENT FILING DATE:  2003-11-12
;  PRIOR APPLICATION NUMBER: 60/427,841
;  PRIOR FILING DATE: 2002-11-20
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
;   LENGTH: 74
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-718-495-20

  Query Match             100.0%;  Score 110;  DB 4;  Length 74;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              ||||||||||||||||||||
Db          1 FKDPNAPKRLPSAFFLFCSE 20


RESULT 14
US-10-718-495-53
; Sequence 53, Application US/10718495
; Publication No. US20040141948A1
; GENERAL INFORMATION:
;  APPLICANT: O'Keefe, Theresa L.
;  TITLE OF INVENTION: USE OF HMGB FRAGMENTS AS
;  TITLE OF INVENTION:  ANTI-INFLAMMATORY AGENTS
;  FILE REFERENCE: 3258.1009-001
;  CURRENT APPLICATION NUMBER: US/10/718,495
;  CURRENT FILING DATE:  2003-11-12
;  PRIOR APPLICATION NUMBER: 60/427,841
;  PRIOR FILING DATE: 2002-11-20
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53
;   LENGTH: 74
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-718-495-53

  Query Match             100.0%;  Score 110;  DB 4;  Length 74;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              ||||||||||||||||||||
Db          1 FKDPNAPKRLPSAFFLFCSE 20


RESULT 15
US-10-717-984-20
; Sequence 20, Application US/10717984
; Publication No. US20040156851A1
; GENERAL INFORMATION:
;  APPLICANT: Newman, Walter
;  TITLE OF INVENTION: HMGB1 COMBINATION THERAPIES
;  FILE REFERENCE: 3258.1008-001
;  CURRENT APPLICATION NUMBER: US/10/717,984
;  CURRENT FILING DATE:  2003-11-20
;  PRIOR APPLICATION NUMBER: 60/427,846
;  PRIOR FILING DATE: 2002-11-20
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
;   LENGTH: 74
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-717-984-20

  Query Match             100.0%;  Score 110;  DB 4;  Length 74;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              ||||||||||||||||||||
Db          1 FKDPNAPKRLPSAFFLFCSE 20


Search completed: April  6, 2006, 10:32:46
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Job time : 20.0132 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 6, 2006, 10:28:08 ; Search time 2.5 Seconds
(without alignments)
249.536 Million cell updates/sec

Title: US-10-717-984-23
Perfect score: 110
Sequence: 1 FKDPNAPKRLPSAFFLFCSE 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 184161

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
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2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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7: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	103	93.6	215	6	US-10-821-234-1443	Sequence 1443, Ap
2	103	93.6	215	7	US-11-186-422-11	Sequence 11, Appl
3	103	93.6	215	7	US-11-186-422-12	Sequence 12, Appl
4	97	88.2	169	6	US-10-821-234-1234	Sequence 1234, Ap
5	97	88.2	879	7	US-11-169-041-192	Sequence 192, App
6	79	71.8	69	7	US-11-186-422-14	Sequence 14, Appl
7	79	71.8	141	7	US-11-087-099-3073	Sequence 3073, Ap
8	77	70.0	160	7	US-11-087-099-1105	Sequence 1105, Ap
9	75	68.2	106	7	US-11-087-099-7075	Sequence 7075, Ap
10	75	68.2	141	7	US-11-087-099-9185	Sequence 9185, Ap
11	75	68.2	142	7	US-11-087-099-4976	Sequence 4976, Ap
12	75	68.2	152	7	US-11-087-099-313	Sequence 313, App
13	75	68.2	152	7	US-11-172-740-1565	Sequence 1565, Ap
14	75	68.2	152	7	US-11-172-740-1566	Sequence 1566, Ap
15	73	66.4	149	7	US-11-087-099-3510	Sequence 3510, Ap
16	73	66.4	149	7	US-11-172-740-1571	Sequence 1571, Ap
17	72	65.5	137	7	US-11-096-568A-3511	Sequence 3511, Ap
18	72	65.5	146	7	US-11-172-740-1569	Sequence 1569, Ap
19	72	65.5	154	7	US-11-087-099-2474	Sequence 2474, Ap
20	72	65.5	154	7	US-11-172-740-1570	Sequence 1570, Ap
21	72	65.5	164	7	US-11-096-568A-3510	Sequence 3510, Ap
22	71	64.5	124	7	US-11-096-568A-9681	Sequence 9681, Ap
23	71	64.5	140	7	US-11-172-740-1564	Sequence 1564, Ap
24	71	64.5	162	7	US-11-096-568A-9680	Sequence 9680, Ap
25	68	61.8	127	7	US-11-096-568A-15615	Sequence 15615, A
26	68	61.8	154	7	US-11-096-568A-15614	Sequence 15614, A
27	64	58.2	93	7	US-11-087-099-869	Sequence 869, App
28	64	58.2	93	7	US-11-087-099-9518	Sequence 9518, Ap
29	64	58.2	125	7	US-11-172-740-1563	Sequence 1563, Ap
30	64	58.2	145	7	US-11-172-740-1572	Sequence 1572, Ap
31	63	57.3	99	7	US-11-087-099-2564	Sequence 2564, Ap
32	63	57.3	446	7	US-11-087-099-370	Sequence 370, App
33	61	55.5	99	7	US-11-087-099-10060	Sequence 10060, A
34	58	52.7	92	7	US-11-087-099-8838	Sequence 8838, Ap
35	58	52.7	108	7	US-11-087-099-6594	Sequence 6594, Ap
36	56.5	51.4	139	7	US-11-096-568A-13611	Sequence 13611, A
37	56	50.9	92	7	US-11-087-099-10535	Sequence 10535, A
38	56	50.9	139	7	US-11-096-568A-26884	Sequence 26884, A
39	56	50.9	149	7	US-11-087-099-11987	Sequence 11987, A
40	56	50.9	187	7	US-11-096-568A-26883	Sequence 26883, A
41	56	50.9	487	7	US-11-087-099-11126	Sequence 11126, A
42	56	50.9	502	7	US-11-087-099-8879	Sequence 8879, Ap
43	53	48.2	372	7	US-11-087-099-6977	Sequence 6977, Ap
44	51	46.4	310	7	US-11-087-099-4210	Sequence 4210, Ap
45	50	45.5	298	7	US-11-087-099-2173	Sequence 2173, Ap

ALIGNMENTS

RESULT 1
US-10-821-234-1443
; Sequence 1443, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1443
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1443

Query Match 93.6%; Score 103; DB 6; Length 215;
Best Local Similarity 95.0%; Pred. No. 3.2e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              ||||||||| ||||||||||
Db         89 FKDPNAPKRPPSAFFLFCSE 108
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RESULT 2
US-11-186-422-11
; Sequence 11, Application US/11186422
; Publication No. US20060057679A1
; GENERAL INFORMATION:
; APPLICANT: Critical Therapeutics, Inc.
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Luciano, Peter
; APPLICANT: Qin, Shixin
; TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
; FILE REFERENCE: 3258.1021-003
; CURRENT APPLICATION NUMBER: US/11/186,422
; CURRENT FILING DATE: 2005-07-20
; PRIOR APPLICATION NUMBER: 60/589,678
; PRIOR FILING DATE: 2004-07-20
; NUMBER OF SEQ ID NOS: 34

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;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-186-422-11

  Query Match             93.6%;  Score 103;  DB 7;  Length 215;
  Best Local Similarity   95.0%;  Pred. No. 3.2e-09;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              ||||||||| ||||||||||
Db         89 FKDPNAPKRPPSAFFLFCSE 108


RESULT 3
US-11-186-422-12
; Sequence 12, Application US/11186422
; Publication No. US20060057679A1
; GENERAL INFORMATION:
;  APPLICANT: Critical Therapeutics, Inc.
;  APPLICANT:  O'Keefe, Theresa
;  APPLICANT:  Luciano, Peter
;  APPLICANT:  Qin, Shixin
;  TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
;  FILE REFERENCE: 3258.1021-003
;  CURRENT APPLICATION NUMBER: US/11/186,422
;  CURRENT FILING DATE:  2005-07-20
;  PRIOR APPLICATION NUMBER: 60/589,678
;  PRIOR FILING DATE: 2004-07-20
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-11-186-422-12

  Query Match             93.6%;  Score 103;  DB 7;  Length 215;
  Best Local Similarity   95.0%;  Pred. No. 3.2e-09;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              ||||||||| ||||||||||
Db         89 FKDPNAPKRPPSAFFLFCSE 108


RESULT 4
US-10-821-234-1234
; Sequence 1234, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
;  APPLICANT: Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  APPLICANT:  Andarmani, Susan
;  APPLICANT:  Tang, Y. Tom
;  TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
;  FILE REFERENCE: 821A
;  CURRENT APPLICATION NUMBER: US/10/821,234
;  CURRENT FILING DATE:  2004-04-07
;  PRIOR APPLICATION NUMBER: US 60/462,047
;  PRIOR FILING DATE: 2003-04-07
;  NUMBER OF SEQ ID NOS: 1704
;  SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1234
;   LENGTH: 169
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(169)
;   OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-821-234-1234

  Query Match             88.2%;  Score 97;  DB 6;  Length 169;
  Best Local Similarity   94.7%;  Pred. No. 2.3e-08;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 KDPNAPKRLPSAFFLFCSE 20
              |||||||| ||||||||||
Db         77 KDPNAPKRPPSAFFLFCSE 95


RESULT 5
US-11-169-041-192
; Sequence 192, Application US/11169041
; Publication No. US20060019284A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
;  TITLE OF INVENTION:  COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
;  TITLE OF INVENTION:  KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: 10001 NP
;  CURRENT APPLICATION NUMBER: US/11/169,041
;  CURRENT FILING DATE:  2005-06-28
;  PRIOR APPLICATION NUMBER: 60/584,405
;  PRIOR FILING DATE: 2004-06-30
;  NUMBER OF SEQ ID NOS: 527
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 192
;   LENGTH: 879
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-169-041-192

  Query Match             88.2%;  Score 97;  DB 7;  Length 879;
  Best Local Similarity   90.0%;  Pred. No. 1.2e-07;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 FKDPNAPKRLPSAFFLFCSE 20
              ||||||||| | ||||||||
Db        763 FKDPNAPKRPPLAFFLFCSE 782


RESULT 6
US-11-186-422-14
; Sequence 14, Application US/11186422
; Publication No. US20060057679A1
; GENERAL INFORMATION:
;  APPLICANT: Critical Therapeutics, Inc.
;  APPLICANT:  O'Keefe, Theresa
;  APPLICANT:  Luciano, Peter
;  APPLICANT:  Qin, Shixin
;  TITLE OF INVENTION: RAGE PROTEIN DERIVATIVES
;  FILE REFERENCE: 3258.1021-003
;  CURRENT APPLICATION NUMBER: US/11/186,422
;  CURRENT FILING DATE:  2005-07-20
;  PRIOR APPLICATION NUMBER: 60/589,678
;  PRIOR FILING DATE: 2004-07-20
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 69
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-186-422-14

  Query Match             71.8%;  Score 79;  DB 7;  Length 69;
  Best Local Similarity   93.8%;  Pred. No. 7.1e-06;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 NAPKRLPSAFFLFCSE 20
              ||||| ||||||||||
Db          1 NAPKRPPSAFFLFCSE 16
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RESULT 7
US-11-087-099-3073
; Sequence 3073, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3073
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Canavalia gladiata
US-11-087-099-3073

Query Match 71.8%; Score 79; DB 7; Length 141;
Best Local Similarity 78.9%; Pred. No. 1.4e-05;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KDPNAPKRLPSAFFLFCSE 20
|||| ||| |||||:| ||
Db 32 KDPNKPKRPPSAFFVFMSE 50

RESULT 8
US-11-087-099-1105
; Sequence 1105, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1105
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Hordeum vulgare subsp. vulgare
US-11-087-099-1105

Query Match 70.0%; Score 77; DB 7; Length 160;
Best Local Similarity 73.7%; Pred. No. 3.4e-05;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 KDPNAPKRLPSAFFLFCSE 20
|||| ||| |||||:| |
Db 37 KDPNKPKRAPSAFFVFMGE 55

RESULT 9
US-11-087-099-7075
; Sequence 7075, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 7075
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Narcissus pseudonarcissus
US-11-087-099-7075

Query Match 68.2%; Score 75; DB 7; Length 106;
Best Local Similarity 73.7%; Pred. No. 4.7e-05;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 KDPNAPKRLPSAFFLFCSE 20
|||| ||| |||||:| |
Db 41 KDPNKPKRPPSAFFVFMEE 59

RESULT 10
US-11-087-099-9185
; Sequence 9185, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9185
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Solanum tuberosum
US-11-087-099-9185

Query Match 68.2%; Score 75; DB 7; Length 141;
Best Local Similarity 73.7%; Pred. No. 6.3e-05;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 KDPNAPKRLPSAFFLFCSE 20
|||| ||| |||||:| |
Db 31 KDPNKPKRPPSAFFVFMEE 49

RESULT 11
US-11-087-099-4976
; Sequence 4976, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 4976
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-11-087-099-4976

Query Match 68.2%; Score 75; DB 7; Length 142;
Best Local Similarity 73.7%; Pred. No. 6.3e-05;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 KDPNAPKRLPSAFFLFCSE 20
|||| ||| |||||:| |
Db 31 KDPNKPKRPPSAFFVFMEE 49

RESULT 12
US-11-087-099-313
; Sequence 313, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 313
; LENGTH: 152
; TYPE: PRT

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;   ORGANISM: Glycine max
US-11-087-099-313

  Query Match             68.2%;  Score 75;  DB 7;  Length 152;
  Best Local Similarity   73.7%;  Pred. No. 6.7e-05;
  Matches   14;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 KDPNAPKRLPSAFFLFCSE 20
              |||| ||| |||||:|  |
Db         39 KDPNKPKRPPSAFFVFMEE 57


RESULT 13
US-11-172-740-1565
; Sequence 1565, Application US/11172740
; Publication No. US20060057724A1
; GENERAL INFORMATION:
;  APPLICANT: MASCIA, Peter
;  APPLICANT:  ALEXANDROV, Nickolai
;  APPLICANT:  BROVER, Vyacheslav
;  TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR
;  TITLE OF INVENTION:  PLANT CHARACTERISTICS AND PHENOTYPES
;  FILE REFERENCE: 2750-1602PUS2
;  CURRENT APPLICATION NUMBER: US/11/172,740
;  CURRENT FILING DATE:  2005-06-30
;  PRIOR APPLICATION NUMBER: 60/583,621
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/584,829
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/584,800
;  PRIOR FILING DATE: 2004-06-30
;  NUMBER OF SEQ ID NOS: 2523
; SEQ ID NO 1565
;   LENGTH: 152
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(152)
;   OTHER INFORMATION: Ceres CLONE ID no. 721511
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: Utility: Useful for increasing seed/fruit yield or modifying frui
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: Utility: Useful for making ornamental plants with modified flower
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: Utility: Useful for making ornamental plants with modified leaves
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: Utility: Useful for making plants sterile and for genetic confine
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: Utility: Useful for making plants with increased biomass
US-11-172-740-1565

  Query Match             68.2%;  Score 75;  DB 7;  Length 152;
  Best Local Similarity   73.7%;  Pred. No. 6.7e-05;
  Matches   14;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 KDPNAPKRLPSAFFLFCSE 20
              |||| ||| |||||:|  |
Db         39 KDPNKPKRPPSAFFVFMEE 57


RESULT 14
US-11-172-740-1566
; Sequence 1566, Application US/11172740
; Publication No. US20060057724A1
; GENERAL INFORMATION:
;  APPLICANT: MASCIA, Peter
;  APPLICANT:  ALEXANDROV, Nickolai
;  APPLICANT:  BROVER, Vyacheslav
;  TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR N
;  TITLE OF INVENTION:  PLANT CHARACTERISTICS AND PHENOTYPES
;  FILE REFERENCE: 2750-1602PUS2
;  CURRENT APPLICATION NUMBER: US/11/172,740
;  CURRENT FILING DATE:  2005-06-30
;  PRIOR APPLICATION NUMBER: 60/583,621
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/584,829
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: 60/584,800
;  PRIOR FILING DATE: 2004-06-30
;  NUMBER OF SEQ ID NOS: 2523
; SEQ ID NO 1566
;   LENGTH: 152
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(152)
;   OTHER INFORMATION: Public GI no. 18645
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: Utility: Useful for increasing seed/fruit yield or modifying fruit
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: Utility: Useful for making ornamental plants with modified flowers
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: Utility: Useful for making ornamental plants with modified leaves
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: Utility: Useful for making plants sterile and for genetic confinem
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION:
;   OTHER INFORMATION: Utility: Useful for making plants with increased biomass
US-11-172-740-1566

  Query Match             68.2%;  Score 75;  DB 7;  Length 152;
  Best Local Similarity   73.7%;  Pred. No. 6.7e-05;
  Matches   14;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 KDPNAPKRLPSAFFLFCSE 20
              |||| ||| |||||:|  |
Db         39 KDPNKPKRPPSAFFVFMEE 57


RESULT 15
US-11-087-099-3510
; Sequence 3510, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
;  CURRENT FILING DATE:  2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3510
;   LENGTH: 149
;   TYPE: PRT
;   ORGANISM: Vicia faba
US-11-087-099-3510
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Query Match 66.4%; Score 73; DB 7; Length 149;
Best Local Similarity 68.4%; Pred. No. 0.00014;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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Qy          2 KDPNAPKRLPSAFFLFCSE 20
              |||| ||| |||||:| ::
Db         40 KDPNKPKRPPSAFFVFMAD 58
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Search completed: April 6, 2006, 10:33:30
Job time : 3.5 secs